

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 11:04:58 ; Search time 4437 Seconds
(without alignments)
11338.802 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	8					Description
	No.	Score	Query Match	Length	ID	
	1	1559.6	75.3	3859	11 AK014464	AK014464 Mus muscu
	2	1554	75.1	3634	11 AK041285	AK041285 Mus muscu
	3	1554	75.1	3877	11 AK033112	AK033112 Mus muscu
	4	1552.4	75.0	4046	11 AK049626	AK049626 Mus muscu
	5	1552.4	75.0	4101	11 AK046175	AK046175 Mus muscu
	6	1530.4	73.9	3805	11 AK082230	AK082230 Mus muscu
	7	1514.2	73.1	3880	11 AK080498	AK080498 Mus muscu
	8	1347.2	65.1	4048	11 AK082317	AK082317 Mus muscu
	9	1068.4	51.6	3147	11 AK079814	AK079814 Mus muscu
	10	991.6	47.9	1114	9 AF150387	AF150387 AF150387
	11	960.8	46.4	2504	11 AK014390	AK014390 Mus muscu
c	12	935.8	45.2	1025	13 BX463709	BX463709 BX463709
	13	819.6	39.6	913	13 BQ949536	BQ949536 AGENCOURT
	14	791.2	38.2	928	13 BU557282	BU557282 AGENCOURT
c	15	787.4	38.0	858	9 AL570757	AL570757 AL570757
	16	763.8	36.9	950	13 BU502697	BU502697 AGENCOURT
	17	751.8	36.3	932	13 BU148788	BU148788 AGENCOURT
c	18	746	36.0	747	12 BQ018588	BQ018588 UI-H-DH1-
	19	740.6	35.8	1059	12 BI084083	BI084083 602869445
c	20	725.2	35.0	956	13 BX433493	BX433493 BX433493
c	21	723.8	35.0	865	12 BI084878	BI084878 602869445
	22	713.8	34.5	761	12 BM016288	BM016288 603642760
	23	705.6	34.1	797	13 BU193314	BU193314 AGENCOURT
	24	690.2	33.3	904	10 BE378929	BE378929 601237528
	25	689.4	33.3	826	13 BU182102	BU182102 AGENCOURT
c	26	681.4	32.9	718	10 BF057767	BF057767 7k53e11.x
	27	679.4	32.8	802	13 BU613719	BU613719 UI-M-EW0-
	28	675.6	32.6	945	13 BQ669630	BQ669630 AGENCOURT
	29	657.8	31.8	684	10 BF338951	BF338951 602036021
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	31	633	30.6	789	10 BF204338	BF204338 601866411
	32	631.2	30.5	1001	13 BU128383	BU128383 603113984
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	34	624	30.1	635	10 BE296749	BE296749 601175134
	35	597	28.8	684	9 AV725513	AV725513 AV725513
	36	595	28.7	623	12 BI828125	BI828125 603075385
	37	591.6	28.6	862	12 BI157614	BI157614 602922587
	38	587.6	28.4	644	10 BE783981	BE783981 601472451
c	39	585.8	28.3	614	13 BU078439	BU078439 in26c07.x
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c	41	574.2	27.7	649	10 BE837592	BE837592 RC2-FN009
c	42	574	27.7	589	14 CA444983	CA444983 UI-H-DT1-
	43	561	27.1	633	13 BU073919	BU073919 in26c07.y
	44	558	27.0	939	10 BF203806	BF203806 601868788
	45	540.8	26.1	624	13 BU708350	BU708350 UI-M-FC0-

ALIGNMENTS

RESULT 1
AK014464
LOCUS AK014464 3859 bp mRNA linear HTC 05-DEC-2002
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04 product:beta-site APP cleaving enzyme, full insert sequence.
ACCESSION AK014464
VERSION AK014464.1 GI:12852334
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3859)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES Location/Qualifiers
source 1. .3859

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/strain="C57BL/6J"
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/db_xref="MGI:1896726"
/db_xref="taxon:10090"
/clone="4122401C04"
/tissue_type="head"
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/dev_stage="16 days embryo"
430..1935

CDS
/note="unnamed protein product; beta-site APP cleaving
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BASE COUNT 873 a 1082 c 1028 g 876 t
ORIGIN

Query Match 75.3%; Score 1559.6; DB 11; Length 3859;
Best Local Similarity 87.5%; Pred. No. 6.2e-193;
Matches 1798; Conservative 0; Mismatches 244; Indels 12; Gaps 8;

Qy	1	ATGGCCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGTCTGCCCTGCCAC	60
Db	430	ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCCTGCCAG	489
Qy	61	GGCAGCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Db	490	GGAACCCATCTCGGCATCCGGCTGCCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC	549
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGAGCTTT	180
Db	550	CTGAGGCTGCCCCGGGAGACCGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT	609
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	610	GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC	669
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA	300
Db	670	GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACCTTGCA	729
Qy	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360

Db	730	GTGGGGGCTGCCCCACACCCTTTCTGTCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	789
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	790	TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGAA	849
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	850	CTGGGCACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT	909
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	910	GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACTGGGAGGGCATCCTA	969
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	970	GGGCTGGCCTATGCTGAGATTGCCAGGCCGACGACTCTTTGGAGCCCTTCTTTGACTCC	1029
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
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Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	1090	CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC	1149
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	1150	GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT	1209
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
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Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
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Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	1330	GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCTGGAT	1389
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Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
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Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
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Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
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Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1630	GGTTTCTATGTCGTCTTCGATCGAGCCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC	1689
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Db	1690	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGTCCGTTTGTACGGCAGACATG	1749
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
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Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1810	GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG	1869
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1870	CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1929
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1930	AAGTAAGGAGGCCCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTTCC	1989
Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1990	CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	2049
Qy	1619	CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC	1678
Db	2050	CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC	2108
Qy	1679	AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATA	1738
Db	2109	AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA	2168
Qy	1739	CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC	1798
Db	2169	TCCTTAGACACCACAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC	2227
Qy	1799	CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAG	1858
Db	2228	CTCTGCCCCAGCGTCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG	2284
Qy	1859	AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA	1918
Db	2285	AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA	2343
Qy	1919	AGAGACCAAGCTTGTTCCTTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA	1978
Db	2344	AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGA--AAGTGAAGTTTGCCA	2400
Qy	1979	TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT	2038
Db	2401	GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT	2459

Qy 2039 GAATTAAAAAAA 2052
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Db 2460 GAGATAACAAGAA 2473

RESULT 2

AK041285

LOCUS AK041285 3634 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530097B07 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK041285

VERSION AK041285.1 GI:26334342

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,

Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3634)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
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RESULT 3

AK033112

LOCUS AK033112 3877 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 15 days embryo male testis cDNA, RIKEN full-length

enriched library, clone:8030431G04 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK033112

VERSION AK033112.1 GI:26328834

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
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 REFERENCE 6 (bases 1 to 3877)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.go.jp/
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BASE COUNT 877 a 1090 c 1030 g 880 t
ORIGIN

Query Match 75.1%; Score 1554; DB 11; Length 3877;
Best Local Similarity 87.7%; Pred. No. 3.3e-192;
Matches 1801; Conservative 0; Mismatches 240; Indels 13; Gaps 9;

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Qy	661	CCCCTCAACCAAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGGTATC	720
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Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

- REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
- REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
- REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
- REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
- REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4046)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .4046
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM_DB:C530008K17"
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 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="12 days embryo"

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 /note="unnamed protein product; beta-site APP cleaving enzyme (MGD|MGI:1346542, GB|NM_011792, evidence: BLASTN, 98%, match=3874)
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 /translation="MAPALHWLLLVGSGMLPAQGTHLGIRLPLRSGLAGPPLGLRLP
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 GFPLNQTEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYVEIIVRVEINGQDLKM
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BASE COUNT 951 a 1102 c 1056 g 937 t
ORIGIN

Query Match 75.0%; Score 1552.4; DB 11; Length 4046;
Best Local Similarity 87.6%; Pred. No. 5.2e-192;
Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaide,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4101)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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BASE COUNT 964 a 1118 c 1066 g 953 t

ORIGIN

Query Match 75.0%; Score 1552.4; DB 11; Length 4101;
Best Local Similarity 87.6%; Pred. No. 5.1e-192;
Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
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 AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
 Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
 Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
 and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3805)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,


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URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES
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Db	1948	TCAAGTAAGGAGGCCCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTT	2007
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RESULT 7

AK080498

LOCUS AK080498 3880 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730059K08 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK080498

VERSION AK080498.1 GI:26099278

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,

Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3880)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
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ORIGIN

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Matches 1797; Conservative 0; Mismatches 243; Indels 17; Gaps 12;

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RESULT 8

AK082317

LOCUS AK082317 4048 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230037E16 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK082317

VERSION AK082317.1 GI:26349644

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

TITLE Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
 Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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 Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
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 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
 and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 4048)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,

Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source Location/Qualifiers

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BASE COUNT 952 a 1103 c 1045 g 948 t

ORIGIN

Query Match 65.1%; Score 1347.2; DB 11; Length 4048;

Best Local Similarity 82.6%; Pred. No. 1.7e-165;

Matches 1697; Conservative 0; Mismatches 243; Indels 114; Gaps 9;

Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60

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 Qy 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
 Db 1231 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 1290
 Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCAACCAACCTTCGTTTGCCCAAGAAA 900

Db 1291 ----- 1290

Qy 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT 960
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Db 1291 -----ACGGAGAAGTCCCGGAT 1308

Qy 961 GGTCTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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Db 1309 GGCTTTTGGCTAGGGGAACAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT 1368

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Db 1369 TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC 1428

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Db 1429 ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT 1488

Qy 1141 TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Db 1489 TACAAGTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA 1548

Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC 1260
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Db 1549 GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAAGCGAATTGGCTTTGCTGTGTCAGCGCTTGC 1608

Qy 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
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Db 1609 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGTCCGTTTGTACGGCAGACATG 1668

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Db 1669 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACACTTATGACCATAGCCTAT 1728

Qy 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG 1440
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Db 1729 GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTGTCAGTGG 1788

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Db 1849 AAGTAAGGAGGCCCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTTCC 1908

Qy 1561 CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT 1618
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Db 1909 CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT 1968

Qy 1619 CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC 1678
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Db 1969 CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC 2027

Qy 1679 AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATA 1738
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Db 2028 AGGGCTTGACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 2087

Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
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Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
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 Db 2204 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 2262

Qy 1919 AGAGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
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 Db 2263 AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGA--AAGTGAAGTTTGCCA 2319

Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
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 Db 2320 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2378

Qy 2039 GAATTAAAAAAA 2052
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 Db 2379 GAGATAAACAAGAA 2392

RESULT 9

AK079814

LOCUS AK079814 3147 bp mRNA linear HTC 05-DEC-2002

DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430076B07 product:beta-site APP cleaving enzyme, full insert sequence.

ACCESSION AK079814

VERSION AK079814.1 GI:26098773

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3147)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers
source 1. .3147
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A430076B07"
/db_xref="taxon:10090"
/clone="A430076B07"
/tissue_type="thymus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
misc_feature 1. .3147
/note="beta-site APP cleaving enzyme (MGD|MGI:1346542,
GB|NM_011792, evidence: BLASTN, 98%, match=3874)"

BASE COUNT 738 a 840 c 791 g 778 t
ORIGIN

Query Match 51.6%; Score 1068.4; DB 11; Length 3147;
Best Local Similarity 86.3%; Pred. No. 2.1e-129;
Matches 1286; Conservative 0; Mismatches 191; Indels 13; Gaps 9;

Qy 565 AGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCC 624
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Db 282 AGGCCCCGACGACTCTTTGGAGCCCTTCTTTGACTCCCTGGTGAAGCAGACCCACATTCCC 341

Qy 625 AACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTG 684
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Db 342 AACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTCCCCCTCAACCAGACCGAGGCACTG 401

Qy 685 GCCTCTGTCTGGAGGGAGCATGATCATTTGGAGGTATCGACCACTCGCTGTACACAGGCAGT 744
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Db 402 GCCTCGGTGGGAGGGAGCATGATCATTTGGTGGTATCGACCACTCGCTATACACGGGCAGT 461

Qy 745 CTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGAGGT'CAT'CATTTGTGCGGGTGGAG 804
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Db 462 CTCTGGTACACACCCATCCGGCGGGAGTGGTATTATGAAGTGATCATTGTACGTGTGGAA 521

Qy 805 ATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTG 864
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Db 522 ATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAGTACAACCTACGACAAGAGCATTGTG 581

Qy 865 GACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCC 924
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Qy 925 ATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGAGAGCAGCTG 984

Db	642	ATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGATGGCTTTTGGCTAGGGGAGCAGCTG	701
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Db	762	ATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACCATCCTTCCCTCAGCAATACCTACGG	821
Qy	1105	CCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGGCCATCTCACAGTCA	1164
Db	822	CCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGTTACAAGTTCGCTGTCTCACAGTCA	881
Qy	1165	TCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGG	1224
Db	882	TCCACGGGCACTGTTATGGGAGCCGTCATCATGGAAGGTTTCTATGTCGCTCTTCGATCGA	941
Qy	1225	GCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACG	1284
Db	942	GCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACG	1001
Qy	1285	GCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCA	1344
Db	1002	GCGGCAGTGGAAGGTCCGTTTGTACGGCAGACATGGAAGACTGTGGCTACAACATTCCC	1061
Qy	1345	CAGACAGATGAGTCAACCCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTC	1404
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Qy	1405	TTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAG	1464
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Qy	1465	CAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAA	1524
Db	1182	CAGCACGATGACTTTGCTGATGACATCTCCCTGCTCAAGTAAGGAGGCCCGTGGGCAGAT	1241
Qy	1525	GATAGAGATTCCCTTGGACCACACCTCCGTGGTTCACTTTGGTCACA--AGTAGGAGACA	1582
Db	1242	GATGGAGACGCCCTTGGACCACATCTGGGTGGTTCCCTTTGGTCACATGAGTTGGAGCTA	1301
Qy	1583	CAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCCCCACCCACCAAATGCCTCTGCC	1642
Db	1302	TGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCCTACCAACCTGCCAATGCTTCTGGC	1361
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Qy	1703	AAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGT	1762
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Db      1481 -TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACCCTCTGCCCAGCA-TCCTTTAGAGT 1538
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Qy      1943 GGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATTGCTTTAGAGACAGGGACTGTA 2002
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Qy      2003 TAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGAATTAACAAAAA 2052
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Db      1712 GACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTTGAGATAAACAAGAA 1760

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RESULT 10

AF150387

LOCUS AF150387 1114 bp mRNA linear EST 22-JUN-1999

DEFINITION AF150387 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone
CBMAPH03, mRNA sequence.

ACCESSION AF150387

VERSION AF150387.1 GI:5133823

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1114)

AUTHORS Ye,M., Zhang,Q.H., Zhou,J., Shen,Y., Wu,X.Y., Guan,Z.Q., Wang,L.,
Fan,H.Y., Mao,Y.F., Dai,M., Huang,Q.H., Chen,S.J. and Chen,Z.

TITLE Human mRNA from cd34+ stem cells

JOURNAL Unpublished

COMMENT Contact: Ye M

Shanghai Institute of Hematology
Shanghai Second Medical University, Rui-Jin Hospital
197 Rui-Jin Road II, Shanghai, 200025, P. R. China
Email: zchen@stn.sh.cn.

FEATURES Location/Qualifiers

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source      1. .1114
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BASE COUNT 275 a 300 c 286 g 253 t

ORIGIN

Query Match 47.9%; Score 991.6; DB 9; Length 1114;

Best Local Similarity 97.4%; Pred. No. 3.2e-119;

Matches 1093; Conservative 0; Mismatches 19; Indels 10; Gaps 8;

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Qy	952	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT	1011
Db	241	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT	300
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Db	479	ATCATGGAGGGCTTCTACCGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGT	538
Qy	1251	CAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTAC	1310
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Qy	1371	CATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGT	1430
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Qy	1431	GTGTCAG-TGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACA	1489
Db	717	GTGTCAGATGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTATGCTGATGACA	776
Qy	1490	TCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACC	1549
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TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
 Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
 Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
 Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
 Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
 Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
 Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
 Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
 Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
 Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
 Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
 Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
 Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
 Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
 Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
 Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
 Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
 Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
 and Hayashizaki,Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 2504)
 AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
 Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
 Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
 Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
 Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
 Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
 Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
 Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
 Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
 Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
 Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 COMMENT On Dec 10, 2002 this sequence version replaced gi:12852207.
 Please visit our web site (http://genome.gsc.riken.go.jp/) for
 further details.

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FEATURES             Location/Qualifiers
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                        /db_xref="taxon:10090"
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                        /db_xref="MGI:1346542"
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     polyA_site        2504
                        /note="putative"

BASE COUNT            616 a      637 c      631 g      620 t
ORIGIN

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Qy 703 ATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATC 762
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 Db 1 ATGATCATTGGTGGTATCGACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATC 60
 Qy 763 CGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTG 822
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Db	61	CGGCGGGAGTGGTATTATGAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTC	120
Qy	823	AAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACCAAC	882
Db	121	AAGATGGACTGCAAGGAGTACAACACGACAAGAGCATTGTGGACAGTGGGACCACCAAC	180
Qy	883	CTTCGTTTGTCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCC	942
Db	181	CTTCGCTTGTCCCAAGAAAGTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCG	240
Qy	943	ACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGC	1002
Db	241	ACGGAGAAGTTCCCGGATGGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGC	300
Qy	1003	ACCACCCCTTGGAAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAAC	1062
Db	301	ACGACCCCTTGGAAACATTTTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAAT	360
Qy	1063	CAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCC	1122
Db	361	CAGTCCTTCCGCATCACCATCCTTCCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCC	420
Qy	1123	ACGTCCCAAGACGACTGTTTACAAGTTTGGCCATCTCACAGTCATCCACGGGCACTGTTATG	1182
Db	421	ACGTCCCAAGACGACTGTTTACAAGTTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATG	480
Qy	1183	GGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGC	1242
Db	481	GGAGCCGTCATCATGGAAGGTTTCTATGTCGTCTTCGATCGAGCCCGAAAGCGAATTGGC	540
Qy	1243	TTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCT	1302
Db	541	TTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGTCCG	600
Qy	1303	TTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACC	1362
Db	601	TTTGTTACGGCAGACATGGAAGACTGTGGCTACAACATTCCCAGACAGATGAGTCAACA	660
Qy	1363	CTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGC	1422
Db	661	CTTATGACCATAGCCTATGTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGC	720
Qy	1423	CTCATGGTGTGTCAAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCT	1482
Db	721	CTCATGGTATGTCAAGTGGCGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCT	780
Qy	1483	GATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTTGA	1542
Db	781	GATGACATCTCCCTGCTCAAGTAAGGAGGCCCGTGGGCAGATGATGGAGACGCCCTTGA	840
Qy	1543	CCACACCTCCGTGGTTCACTTTGGTCAACA--AGTAGGAGACACAGATGGCACCTGTGGCC	1600
Db	841	CCACATCTGGGTGGTTCCCTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCC	900
Qy	1601	AGAGCACCTCAGGACCCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAG	1660
Db	901	AGAGCACCTCAGGACCCCTACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAA	959

Qy	1661	GCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAACG	1720
Db	960	TCAGGCAAGCTGGATTACAGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGC	1019
Qy	1721	ACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTT	1780
Db	1020	GTTCTGGTGGCAGGAATATCCTTAGACACCACAACTTGAGT-TGGAAATTTTGCTGCTT	1078
Qy	1781	GAAACTTCAGCCCTGAACCTTTGTCCACCATTCCCTTTAAATTCTCCAACCCAAAGTATTC	1840
Db	1079	GAAGCTTCAGCCCTGACCCTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTC	1137
Qy	1841	TTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCT	1900
Db	1138	TTTATGTC---CTTCCAGAAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCT	1193
Qy	1901	GTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAG	1960
Db	1194	GTGGTACCCTGGCAGAGAAAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAG	1252
Qy	1961	AGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTG	2020
Db	1253	A--AAGTGAAGTTTGCCAGTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTG	1309
Qy	2021	GTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAA	2052
Db	1310	GTACAAAGACTGCGTCTTGAGATAAACAAGAA	1341

RESULT 12

LOCUS BX463709 1025 bp mRNA linear EST 22-MAY-2003

DEFINITION BX463709 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone

CS0DN005YN12 3-PRIME, mRNA sequence.

ACCESSION BX463709

VERSION BX463709.1 GI:31033554

KEYWORDS EST.

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM	Homo sapiens
----------	--------------

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1025)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5902.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0DN005DG06NP1&cluster=5902.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

Qy 1545 ACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAG 1604
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 Db 460 ACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAG 401
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 Db 400 CACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTG 341
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 Db 340 GCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTC 281
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 Db 220 CTTCAGCCCTGAACCTTTGTCCACCATTCCCTTTAAATTCTCCAACCCAAAGTATTCTTCT 161
 Qy 1845 TTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGG 1904
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 Db 160 TTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGG 101
 Qy 1905 TACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGA 1964
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 Db 100 TACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAVHCCATAGGAGAGGA 41
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 Db 40 TNCACAGCTTGCTATTTGCTNTAGAGACAGG 10

RESULT 13

BQ949536

LOCUS BQ949536 913 bp mRNA linear EST 21-AUG-2002
 DEFINITION AGENCOURT_8733256 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:6454803
 5', mRNA sequence.

ACCESSION BQ949536

VERSION BQ949536.1 GI:22365014

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 913)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2632 row: h column: 04
High quality sequence stop: 613.

FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6454803"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_101"
 /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
 XhoI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
BASE COUNT 207 a 259 c 232 g 206 t 9 others
ORIGIN

Query Match 39.6%; Score 819.6; DB 13; Length 913;
Best Local Similarity 96.8%; Pred. No. 6e-97;
Matches 864; Conservative 0; Mismatches 26; Indels 3; Gaps 3;

Qy 904 TTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGATGGT 963
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Db 1 TTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGATGGT 60

Qy 964 TTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAACATTTTC 1023
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Qy 1024 CCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATC 1083
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Db 121 CCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATC 180

Qy 1084 CTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTAC 1143
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Db 181 CTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTAC 240

Qy 1144 AAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGC 1203
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Db 241 AAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGC 300

Qy 1204 TTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCAT 1263
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Db 301 TTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCAT 360

Qy 1264 GTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATGGAA 1323
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Db 361 GTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATGGAA 420

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Db      421  ||||| GACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTC 480
Qy      1384 ATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGGCGC 1443
Db      481  ||||| ATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGGCGC 540
Qy      1444 TGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAG 1503
Db      541  ||||| TGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAG 600
Qy      1504 TGAGGAGGCCCATGGGCAGAAGATAGAGATTCCTGGACCACACCTCCGTGGTTCACTT 1563
Db      601  ||||| TGAGGAGGCCCATGGGCAGAAGATAGAGATTCCTGGACCACACCTCCGTGGTTCACTT 660
Qy      1564 TGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCA 1623
Db      661  ||||| TGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCA 720
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Db      721  ||||| CCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGNGTTCCAGGGG 780
Qy      1683 ACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATACTC- 1741
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Qy      1742 TTGGTCACCTCAAATTTAAGTCGGGAAATTCT-GCTGCTTGAAACTTCAGCCC 1793
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RESULT 14

BU557282

LOCUS BU557282 928 bp mRNA linear EST 16-SEP-2002

DEFINITION AGENCOURT_10253167 NIH_MGC_109 Homo sapiens cDNA clone

IMAGE:6585124 5', mRNA sequence.

ACCESSION BU557282

VERSION BU557282.1 GI:22907578

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 928)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

FEATURES

BASE COUNT
ORIGIN

205 a 254 c 251 g 217 t 1 others

[illegible]

Db 454 GCACCACCAACCTTCGTTTGTCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGG 513

Qy 932 CAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCT 991
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Db 514 CAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCT 573

Qy 992 GGCAAGCAGGCACCACCCCTTGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTG 1051
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Db 574 GGCAAGCAGGCACCACCCCTTGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTG 633

Qy 1052 AGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGG 1111
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Db 634 AGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGG 693

Qy 1112 AAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGG 1171
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Db 694 AAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGG 753

Qy 1172 GCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCC--G 1229
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Db 754 GCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGA 813

Qy 1230 AAAACGAATTGGCTTTGCTGTCA-GCGCTTGCCATGTGCACGATGAGTTCAGGACGGC 1286
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Db 814 AAACGAATTGGGCTTTGCTGTCAAGGCGCTTGCCATGTGCACGATGAAGTCAGGGACGC 871

RESULT 15

AL570757/c

LOCUS AL570757 858 bp mRNA linear EST 31-MAY-2003

DEFINITION AL570757 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI022YF22 3-PRIME, mRNA sequence.

ACCESSION AL570757

VERSION AL570757.2 GI:31292174

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 858)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 16, 2001 this sequence version replaced gi:12927378.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5902.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI022DC11NP1&cluster=5902.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI022DC11NP1.

FEATURES Location/Qualifiers

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source          1. .858
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                 /tissue_type="PLACENTA COT 25-NORMALIZED"
                 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                 /note="1st strand cDNA was primed with a NotI-oligo(dT)
                 primer. Five prime end enriched, double-strand cDNA was
                 digested with Not I and cloned into the Not I and EcoR V
                 sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      214 a      205 c      224 g      200 t      15 others
ORIGIN

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Query Match          38.0%; Score 787.4; DB 9; Length 858;
Best Local Similarity 97.2%; Pred. No. 9e-93;
Matches 824; Conservative 5; Mismatches 16; Indels 3; Gaps 3;

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Qy      1148 TTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCT 1207
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Db      845 TTSCCATCTCACATTCATCCAC-GGCACTGTTAT-GGAGCTGTTATCAT-GARGGCTTCT 789

Qy      1208 ACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGC 1267
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Db      788 ACWTTGTCTTTGATCGGGCCCGAAAACGAATTGGYTTGCTRTTCAGCGCTTGCCATGTGC 729

Qy      1268 ACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGACATGGAAGACT 1327
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Db      728 ACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACTTGYACATGGAAGACT 669

Qy      1328 GTGGCTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTATGTCATGG 1387
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Db      668 GTGGCTACAACATTCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTATGTCATGG 609

Qy      1388 CTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGGCGCTGCC 1447
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Db      608 CTGCCATNTGCGCCCTCTTNATGCTGCCACTCTGCCTCATGGTGTGTGAGTGGCGCTGCC 549

Qy      1448 TCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAG 1507
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Db      548 TCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAG 489

Qy      1508 GAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGT 1567
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Db      488 GAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGT 429

Qy      1568 CACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCA 1627
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Qy      1628 CCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGT 1687
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Qy	1748	ACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCTTTGTCCA	1807
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Qy	1808	CCATTCCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGG	1867
Db	188	CCATTCCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGG	129
Qy	1868	CATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAGAGACCAA	1927
Db	128	CATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAGAGWCCAA	69
Qy	1928	GCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATTTGCTTTA	1987
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Qy	1988	GAGACAGG	1995
Db	8	GAGACAGG	1

Search completed: January 21, 2004, 14:43:37
Job time : 4456 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 09:28:36 ; Search time 7650 Seconds
(without alignments)
11069.664 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

		%									
Result		Query									
No.	Score	Match	Length	DB	ID	Description					
1	2070	100.0	2070	6	AX105385	AX105385 Sequence					
2	2070	100.0	2070	6	AX378015	AX378015 Sequence					
3	2070	100.0	2070	6	AX573823	AX573823 Sequence					
4	2068.4	99.9	2070	6	AR224093	AR224093 Sequence					
5	2068.4	99.9	2070	6	AR269224	AR269224 Sequence					
6	2068.4	99.9	2070	6	AX700447	AX700447 Sequence					
7	2068.4	99.9	2070	9	AF200343	AF200343 Homo sapi					
8	2062	99.6	2526	6	AX700446	AX700446 Sequence					
9	2062	99.6	2526	9	AF190725	AF190725 Homo sapi					
10	2052.6	99.2	5878	9	AF201468	AF201468 Homo sapi					
11	2040	98.6	5814	9	AB032975	AB032975 Homo sapi					
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14	2032	98.2	2541	6	AX700452	AX700452 Sequence					
15	2032	98.2	2541	6	E50816	E50816 Aspartate p					
16	2010	97.1	3252	6	AR305033	AR305033 Sequence					
17	2010	97.1	3252	6	AX062111	AX062111 Sequence					
18	2010	97.1	3252	6	AX063201	AX063201 Sequence					
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20	2010	97.1	3252	6	AX700453	AX700453 Sequence					
21	2010	97.1	3252	9	AF200193	AF200193 Homo sapi					
22	1894.2	91.5	5757	6	AX364933	AX364933 Sequence					
23	1887.2	91.2	1977	6	AR224094	AR224094 Sequence					
24	1887.2	91.2	1977	6	AR269225	AR269225 Sequence					
25	1887.2	91.2	1977	6	AX105387	AX105387 Sequence					
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31	1788.8	86.4	1979	6	BD127853	BD127853 Primer fo
32	1788.8	86.4	1979	9	AK075049	AK075049 Homo sapi
33	1706.8	82.5	2174	9	BC036084	BC036084 Homo sapi
34	1655.8	80.0	1746	6	AX616339	AX616339 Sequence
35	1644.8	79.5	1747	6	BD139308	BD139308 Extended
36	1554	75.1	4059	10	BC048189	BC048189 Mus muscu
37	1552.4	75.0	2043	6	AR224095	AR224095 Sequence
38	1552.4	75.0	2043	6	AR269226	AR269226 Sequence
39	1552.4	75.0	2043	6	AX105389	AX105389 Sequence
40	1552.4	75.0	2043	6	AX573827	AX573827 Sequence
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42	1548.4	74.8	3880	10	AF190726	AF190726 Mus muscu
43	1502.8	72.6	1506	6	AX700448	AX700448 Sequence
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ALIGNMENTS

RESULT 1

AX105385

LOCUS AX105385 2070 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 3 from Patent WO0123533.

ACCESSION AX105385

VERSION AX105385.1 GI:13921511

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gurney,M. and Bienkowski,M.J.

TITLE Alzheimer's disease secretase, app substrates therefor, and uses therefor

JOURNAL Patent: WO 0123533-A 3 05-APR-2001;

Pharmacia & Upjohn Company (US)

FEATURES Location/Qualifiers

source 1. .2070
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 476 a 583 c 562 g 449 t

ORIGIN

Query Match 100.0%; Score 2070; DB 6; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1
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CCCAC 60

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Db 1
ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61
GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61
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CTGGGG 120

Qy 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

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Db 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

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TGACC 240

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Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

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Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

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GGAG 420

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Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421
CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAA
CATT 480

Qy 481
GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481
GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541
GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

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Db 541
GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
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Qy 601
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TTC 660

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Db 601
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Qy 661
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TATC 720

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Db 661
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TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

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Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

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Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

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Db 961

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CATT 1020

Qy 1021

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CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

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CTGT 1140

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Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

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GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

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Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

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CATG 1320

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Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

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TAT 1380

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Db 1321

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TAT 1380

Qy 1381

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TGG 1440

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Db 1381

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TGG 1440

Qy 1441

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CTG 1500

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CTG 1500

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TTCA 1560

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Db 1501

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TTCA 1560

Qy 1561

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CTCC 1620

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Db 1561

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CTCC 1620

Qy 1621

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CCAG 1680

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Db 1621

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CCAG 1680

Qy 1681

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TACT 1740

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Db 1681

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TACT 1740

Qy 1741

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CT 1800

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Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

Qy 1801
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1860

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Db 1801
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Qy 1861
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GAAG 1920

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Db 1861
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GAAG 1920

Qy 1921
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ATT 1980

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Db 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 1981
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GA 2040

Qy 2041 ATTA 2070

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Db 2041 ATTA 2070

RESULT 2

AX378015

LOCUS AX378015 2070 bp DNA linear PAT 18-MAR-2002

DEFINITION Sequence 1 from Patent WO0206306.

ACCESSION AX378015

VERSION AX378015.1 GI:19574050

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yan,R., Tomasselli,A.G., Gurney,M.E., Emmons,T.L., Bienkowski,M.J.
and Heinrikson,R.L.

TITLE Substrates and assays for _g(b)-secretase activity

JOURNAL Patent: WO 0206306-A 1 24-JAN-2002;

PHARMACIA & UPJOHN COMPANY (US)

FEATURES Location/Qualifiers

source 1. 2070

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 476 a 583 c 562 g 449 t

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CCCAC 60

Qy 61

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CTGGGG 120

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Db 61

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Qy 121

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AGCTTT 180

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Db 121

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AGCTTT 180

Qy 181

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TGACC 240

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Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

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TGCA 300

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Db 241

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Qy 301

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CACA 360

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Db 301

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CACA 360

Qy 361

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GGAG 420

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Db 361

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GGAG 420

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Db 421

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Qy 481

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CTG 540

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TCT 600

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Db 541

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TCT 600

Qy 601

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TTC 660

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Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
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Qy 661

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TATC 720

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Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

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TTAT 780

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Db 721

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TTAT 780

Qy 781

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GGAG 840

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Db 781

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GGAG 840

Qy 841

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Db 841

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AAA 900

Qy 901

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GAT 960

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Db 901

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GAT 960

Qy 961

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CATT 1020

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Db 961

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Qy 1021

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CC 1080

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Db 1021

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CC 1080

Qy 1081

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CTGT 1140

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Db 1081

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CTGT 1140

Qy 1141

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GAG 1200

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Db 1141

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GAG 1200

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TGC 1260

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Db 1201

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TGC 1260

Qy 1261

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CATG 1320

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Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

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Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

|||||

Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921
AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

|||||

Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 3

AX573823

LOCUS AX573823 2070 bp DNA linear PAT 07-JAN-2003

DEFINITION Sequence 3 from Patent EP1249498.

ACCESSION AX573823

VERSION AX573823.1 GI:27551477

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Gurney,M. and Bienkowski,M.J.

TITLE Alzheimer's disease secretase, app substrates therefor, and uses
therefor

JOURNAL Patent: EP 1249498-A 3 16-OCT-2002;

PHARMACIA & UPJOHN COMPANY (US)

FEATURES Location/Qualifiers

source 1. .2070

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 476 a 583 c 562 g 449 t

ORIGIN

Query Match 100.0%; Score 2070; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

|||||

Db 1801
TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981
TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

|||||

Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 4

AR224093

LOCUS AR224093 2070 bp DNA linear PAT 26-SEP-2002

DEFINITION Sequence 3 from patent US 6440698.

ACCESSION AR224093

VERSION AR224093.1 GI:23332753

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2070)

AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
Yan,R.

TITLE Alzheimer's disease secretase, APP substrates therefor, and uses
therefor

JOURNAL Patent: US 6440698-A 3 27-AUG-2002;

FEATURES Location/Qualifiers

source 1. .2070

/organism="unknown"

BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

Qy 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361
TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCCAACCAAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCCAACCAAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTCCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

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Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

|||||

Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981

TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 5

AR269224

LOCUS AR269224 2070 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 3 from patent US 6500667.

ACCESSION AR269224

VERSION AR269224.1 GI:29700192

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2070)

AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
Yan,R.

TITLE Aspartyl protease 2 (Asp2) antisense oligonucleotides

JOURNAL Patent: US 6500667-A 3 31-DEC-2002;

FEATURES Location/Qualifiers

source 1..2070

/organism="unknown"

BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCAC 60

Qy 61

GGCACCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGG 120

|||||

Db 61

GGCACCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGG
AGCTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGG
AGCTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CAC 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CAC 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATC
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Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

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Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

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TTC 660

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Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

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Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

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Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

Qy 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGA
CATG 1320

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Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

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Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

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Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

|||||

Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTA 2070

|||||

Db 2041 ATTA 2070

RESULT 6

AX700447

LOCUS AX700447 2070 bp DNA linear PAT 03-APR-2003

DEFINITION Sequence 2 from Patent WO03012089.

ACCESSION AX700447

VERSION AX700447.1 GI:29536238

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yon,J., Cleasby,A., Bruinzeel,W.D., Masure,S.L., Tickle,I. and
Sharff,A.

TITLE Crystal structure of beta-site app cleaving enzyme (bace) and use
thereof

JOURNAL Patent: WO 03012089-A 2 13-FEB-2003;

Astex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)

FEATURES Location/Qualifiers

source 1. 2070
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 6; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

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Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

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Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421

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CATT 480

|||||

Db 421

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CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

Qy 661

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TATC 720

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Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

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TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

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TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

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CTGT 1140

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Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

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GAG 1200

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Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

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TGC 1260

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Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

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CATG 1320

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Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGA
CATG 1320

Qy 1321

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TAT 1380

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Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

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TGG 1440

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Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

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CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

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Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

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Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

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Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

Qy 1801
TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

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Db 1801
TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

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Db 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

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Db 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTA 2070

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Db 2041 ATTA 2070

RESULT 7

AF200343

LOCUS AF200343 2070 bp mRNA linear PRI 12-DEC-1999

DEFINITION Homo sapiens chromosome 11 aspartyl protease 2 mRNA, complete cds.

ACCESSION AF200343

VERSION AF200343.1 GI:6561813

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2070)

AUTHORS Yan,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,
Pauley,A.M., Brashier,J.R., Stratman,N.C., Mathews,W.R., Buhl,A.E.,
Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and
Gurney,M.E.

TITLE Membrane-anchored aspartyl protease with Alzheimer's disease
beta-secretase activity

JOURNAL Nature 402 (6761), 533-537 (1999)

MEDLINE 20057170

PUBMED 10591213

REFERENCE 2 (bases 1 to 2070)

AUTHORS Bienkowski,M.J., Shuck,M.E., Slightom,J.L. and Drong,R.F.

TITLE Direct Submission

JOURNAL Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjohn, 301
Henrietta, Kalamazoo, MI 49007, USA

FEATURES Location/Qualifiers

source 1..2070

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/mol_type="mRNA"

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/map="11q23.3-24.1"

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/db_xref="GI:6561814"

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BASE COUNT 476 a 582 c 563 g 449 t

ORIGIN

Query Match 99.9%; Score 2068.4; DB 9; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
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Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

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Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

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Db 241

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TGCA 300

Qy 301

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CACA 360

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Db 301

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CACA 360

Qy 361
TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

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Db 361
TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

Qy 421
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CATT 480

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Db 421
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CATT 480

Qy 481
GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATC
CTG 540

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Db 481
GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATC
CTG 540

Qy 541
GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541
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TCT 600

Qy 601
CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 601
CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661
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TATC 720

|||||

Db 661
CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721
GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781
GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781
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GGAG 840

Qy 841
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AAA 900

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Db 841
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AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 961

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CATT 1020

Qy 1021

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CC 1080

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Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

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CTGT 1140

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Db 1081

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CTGT 1140

Qy 1141

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GAG 1200

|||||

Db 1141

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GAG 1200

Qy 1201

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TGC 1260

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Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

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TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

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TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

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CTG 1500

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Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

|||||

Db 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

|||||

Db 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

|||||

Db 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

|||||

Db 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

|||||

Db 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

Qy 1861

GTAAGTGGCATCACACGCAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 1861

GTAAGTGGCATCACACGCAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

|||||

Db 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

Qy 1981

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

|||||

Db 1981

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 8

AX700446

LOCUS AX700446 2526 bp DNA linear PAT 03-APR-2003

DEFINITION Sequence 1 from Patent WO03012089.

ACCESSION AX700446

VERSION AX700446.1 GI:29536237

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yon,J., Cleasby,A., Bruinzeel,W.D., Masure,S.L., Tickle,I. and
Sharff,A.

TITLE Crystal structure of beta-site app cleaving enzyme (bace) and use
thereof

JOURNAL Patent: WO 03012089-A 1 13-FEB-2003;

Astex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)

FEATURES Location/Qualifiers

source 1. .2526

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 534 a 781 c 715 g 496 t

ORIGIN

Query Match 99.6%; Score 2062; DB 6; Length 2526;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1
ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 454
ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 513

Qy 61
GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 514
GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 573

Qy 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 574
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 633

Qy 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 634
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 693

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 694

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 753

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 754

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 813

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

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Db 814

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 873

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 874

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 933

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATC
CTG 540

|||||

Db 934

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 993

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 994

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 1053

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 1054

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 1113

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 1114

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 1173

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

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Db 1174

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 1233

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 1234

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 1293

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

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Db 1294

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 1353

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

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Db 1354

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 1413

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

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Db 1414

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1473

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

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Db 1474

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1533

Qy 1081

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CTGT 1140

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Db 1534

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1593

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

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Db 1594

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GAG 1653

Qy 1201

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TGC 1260

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Db 1654

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TGC 1713

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGA
CATG 1320

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Db 1714

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGA
CATG 1773

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

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Db 1774

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1833

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

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Db 1834

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1893

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1894

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1953

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

|||||

Db 1954

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 2013

Qy 1561

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CTCC 1620

|||||

Db 2014

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 2073

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

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Db 2074

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 2133

Qy 1681

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 1740

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Db 2134

GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAA
TACT 2193

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 1800

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Db 2194

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC
CT 2253

Qy 1801

TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
1860

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Db 2254

TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
2313

Qy 1861
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

|||||

Db 2314
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 2373

Qy 1921
AGACCAAGCTTGTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

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Db 2374
AGACCAAGCTTGTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 2433

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 2434
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2493

Qy 2041 ATTA 2070

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Db 2494 ATTA 2523

RESULT 9

AF190725

LOCUS AF190725 2526 bp mRNA linear PRI 26-OCT-1999

DEFINITION Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete
cds.

ACCESSION AF190725

VERSION AF190725.1 GI:6118538

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2526)

AUTHORS Vassar,R., Bennett,B.D., Babu-Khan,S., Kahn,S., Mendiaz,E.A.,
Denis,P., Teplow,D.B., Ross,S., Amarante,P., Loeloff,R., Luo,Y.,
Fisher,S., Fuller,J., Edenson,S., Lile,J., Jarosinski,M.A.,
Biere,A.L., Curran,E., Burgess,T., Louis,J.C., Collins,F.,
Treanor,J., Rogers,G. and Citron,M.

TITLE Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
the transmembrane aspartic protease BACE

JOURNAL Science 286 (5440), 735-741 (1999)

MEDLINE 20002972

PUBMED 10531052

REFERENCE 2 (bases 1 to 2526)

AUTHORS Bennett,B.D., Vassar,R. and Citron,M.

TITLE Direct Submission

JOURNAL Submitted (29-SEP-1999) Neuroscience, Amgen Inc., One Amgen Center
Dr., Thousand Oaks, CA 91320-1799, USA

FEATURES Location/Qualifiers

source 1. .2526

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

gene 1. .2526

/gene="BACE"

CDS 454. .1959

/gene="BACE"

/codon_start=1

/product="beta-site APP cleaving enzyme"

/protein_id="AAF04142.1"

/db_xref="GI:6118539"

/translation="MAQALPWLLLWMGAGVLP AHGTQH GIRLPLR SGLGGAPLGLRLP

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GFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKM

DCKEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAG

TTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGT

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BASE COUNT 534 a 781 c 715 g 496 t

ORIGIN

Query Match 99.6%; Score 2062; DB 9; Length 2526;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2065; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG

CCCAC 60

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Db 454

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG

CCCAC 513

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC

CTGGGG 120

|||||

Db 514

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC

CTGGGG 573

Qy 121
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AGCTTT 180

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Db 574
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 633

Qy 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 634
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 693

Qy 241
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

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Db 694
GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 753

Qy 301
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

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Db 754
GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 813

Qy 361
TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

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Db 814

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 873

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 874

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 933

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

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Db 934

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 993

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

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Db 994

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 1053

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

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Db 1054

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 1113

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 720

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Db 1114

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGG
TATC 1173

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

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Db 1174

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 1233

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 1234

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GGAG 1293

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

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Db 1294

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 1353

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

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Db 1354

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 1413

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 1414

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1473

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1474

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1533

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

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Db 1534

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1593

Qy 1141

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GAG 1200

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Db 1594

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1653

Qy 1201

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TGC 1260

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Db 1654

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TGC 1713

Qy 1261

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CATG 1320

|||||

Db 1714

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGA
CATG 1773

Qy 1321

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TAT 1380

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Db 1774

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TAT 1833

Qy 1381

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TGG 1440

|||||

Db 1834

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1893

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1894

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1953

Qy 1501

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 1560

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Db 1954

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 2013

Qy 1561

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 1620

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Db 2014

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACC
CTCC 2073

Qy 1621

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 1680

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Db 2074

CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTT
CCAG 2133

Qy 1681

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TACT 1740

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Db 2134

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TACT 2193

Qy 1741

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 1800

|||||

Db 2194

CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC
CT 2253

Qy 1801

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
1860

|||||

Db 2254

TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
2313

Qy 1861

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 1920

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Db 2314

GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAAG 2373

Qy 1921

AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

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Db 2374

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ATT 2433

Qy 1981

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 2434

TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2493

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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Db 2494 ATTAAAAAAAAAACTAGAAAAAAAAAAAAA 2523

RESULT 10

AF201468

LOCUS AF201468 5878 bp mRNA linear PRI 19-DEC-1999

DEFINITION Homo sapiens APP beta-secretase mRNA, complete cds.

ACCESSION AF201468

VERSION AF201468.1 GI:6601444

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5878)

AUTHORS Sinha,S., Anderson,J.P., Barbour,R., Basi,G.S., Caccavello,R.,
Davis,D., Doan,M., Dovey,H.F., Frigon,N., Hong,J.,
Jacobson-Croak,K., Jewett,N., Keim,P., Knops,J., Lieberburg,I.,
Power,M., Tan,H., Tatsuno,G., Tung,J., Schenk,D., Seubert,P.,
Suomensaari,S., Wang,S., Walker,D., Zhao,J., McConlogue,L. and
John,V.

TITLE Purification and cloning of amyloid precursor protein
beta-secretase from human brain

JOURNAL Nature 402 (6761), 537-540 (1999)

MEDLINE 20057171

PUBMED 10591214

REFERENCE 2 (bases 1 to 5878)

AUTHORS Basi,G.S., Power,M.D., Wang,S., Tatsuno,G., Frigon,N., Doan,M.,
Hong,G., Keim,P., Anderson,J., Sinha,S. and McConlogue,L.M.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-1999) Gene Expression Group, Elan

Pharmaceuticals, Inc., 800 Gateway Blvd., S. San Francisco, CA
94080, USA

FEATURES Location/Qualifiers

source 1. .5878

 /organism="Homo sapiens"

 /mol_type="mRNA"

 /db_xref="taxon:9606"

 /chromosome="11"

 /map="D11S4352"

 /tissue_type="brain"

CDS 455. .1960

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 /note="membrane type aspartyl protease"

 /codon_start=1

 /product="APP beta-secretase"

 /protein_id="AAF18982.1"

 /db_xref="GI:6601445"

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DCKEYNYDKSIVDSGTTNLRLPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAG

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BASE COUNT 1547 a 1518 c 1405 g 1408 t

ORIGIN

Query Match 99.2%; Score 2052.6; DB 9; Length 5878;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2055; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1
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Db 455
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Qy 61
GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
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Db 515
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Qy 121
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Db 575
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Qy 181
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Qy 241

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Db 695

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TGCA 754

Qy 301

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CACA 360

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Db 755

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CACA 814

Qy 361

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Db 815

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GGAG 874

Qy 421

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Db 875

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Qy 481

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Db 935

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Qy 601

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Qy 661

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Db 1115

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Qy 721

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Db 1175

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Db 1235

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Qy 841

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Db 1295

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AAA 1354

Qy 901

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Db 1355

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Qy 961

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Db 1535

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CTGT 1594

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Db 1595

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Qy 1201

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Db 1655

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Db 1775

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Qy 1381

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Db 1835

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TGG 1894

Qy 1441

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CTG 1500

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Db 1895

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CTG 1954

Qy 1501

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TTCA 1560

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Db 1955

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGG
TTCA 2014

Qy 1561

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Db 2015

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CTCC 2074

Qy 1621

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CCAG 1680

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Db 2075

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Qy 1681

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TACT 1740

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Db 2135

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Qy 1741

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CT 1800

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Db 2195

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CT 2254

Qy 1801

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Db 2255

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Qy 1861
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GAAG 1920

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Db 2315
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GAAG 2374

Qy 1921
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCT
ATT 1980

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Db 2375
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ATT 2434

Qy 1981
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT
GA 2040

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Db 2435
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GA 2494

Qy 2041 ATTAAAAAAAAAAAAAAAAA 2059

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Db 2495 ATTAAAAAAAAAACTAGA 2513

RESULT 11

AB032975

LOCUS AB032975 5814 bp mRNA linear PRI 17-MAY-2001

DEFINITION Homo sapiens mRNA for KIAA1149 protein, partial cds.

ACCESSION AB032975

VERSION AB032975.2 GI:14133242

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Hirose, M., Nagase, T., Ishikawa, K., Kikuno, R., Nomura, N. and
Ohara, O.

TITLE Characterization of cDNA clones selected by the GeneMark analysis
from size-fractionated cDNA libraries from human brain

JOURNAL DNA Res. 6 (5), 329-336 (1999)

MEDLINE 20039618

PUBMED 10574461

REFERENCE 2 (bases 1 to 5814)

AUTHORS Ohara, O., Nagase, T. and Kikuno, R.

TITLE Direct Submission

JOURNAL Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL: <http://www.kazusa.or.jp/huge/>, Tel:438-52-3913,
Fax:438-52-3914)

COMMENT On May 17, 2001 this sequence version replaced gi:6330044.

FEATURES Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="fg04087"

/sex="male"

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/clone_lib="pBluescriptII SK plus"

/dev_stage="adult"

/note="vector:pBluescriptII SK plus. This sequence is
replaced that of hg01289 cDNA as a representative cDNA
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/note="Start codon is not identified."

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BASE COUNT 1494 a 1510 c 1404 g 1406 t

ORIGIN

Query Match 98.6%; Score 2040; DB 9; Length 5814;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2054; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Db 503

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
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Qy 120

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Db 563

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Qy 180

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Db 623

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Qy 240

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Db 683

CGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACT
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Qy 300

AGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCA
GCAC 359

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Db 743

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GCAC 802

Qy 360

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GGGA 419

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Db 803

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GGGA 862

Qy 420

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ACAT 479

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Db 863

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ACAT 922

Qy 480

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CCT 539

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Db 923

TGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCAT
CCT 982

Qy 540

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ACTC 599

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Db 983

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ACTC 1042

Qy 600

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CTT 659

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Db 1043

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CTT 1102

Qy 660

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Db 1103

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GTAT 1162

Qy 720

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Db 1163

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Qy 780

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Db 1223

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GGA 1282

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GAA 899

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Db 1283

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GAA 1342

Qy 900

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TGA 959

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Db 1343

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TGA 1402

Qy 960

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ACAT 1019

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Db 1403

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AC 1079

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Db 1463

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AC 1522

Qy 1080

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Db 1523

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ACTG 1582

Qy 1140

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Db 1583

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Qy 1200

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Db 1643

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Qy 1260

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Db 1703

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Qy 1320

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Db 1763

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CTA 1822

Qy 1380

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Db 1823

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GTG 1882

Qy 1440

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GCT 1499

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Db 1883

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GCT 1942

Qy 1500

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GTTC 1559

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Db 1943

GAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTG
GTTC 2002

Qy 1560

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CCTC 1619

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Db 2003

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CCTC 2062

Qy 1620

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Db 2063

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 2122

Qy 1680

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ATAC 1739

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Db 2123

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ATAC 2182

Qy 1740

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CC 1799

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Db 2183

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Qy 1800

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1859

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Db 2243

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Qy 1860

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Db 2303

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GAA 2362

Qy 1920
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Db 2363
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Qy 1980
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Db 2423
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Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

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Db 2483 AATTAAAAAAAAAACTAGA 2502

RESULT 12

AR178469

LOCUS AR178469 2541 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 1 from patent US 6319689.

ACCESSION AR178469

VERSION AR178469.1 GI:20219607

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2541)

AUTHORS Powell,D.J., Chapman,C.G., Murphy,K. and Smith,T.S.

TITLE ASP2

JOURNAL Patent: US 6319689-A 1 20-NOV-2001;

FEATURES Location/Qualifiers

source 1..2541

/organism="unknown"

BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1

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Db 1

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Qy 61

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Db 61

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Qy 121

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Db 121

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Qy 181

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Db 181

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Qy 241

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Db 241

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TGCA 300

Qy 301

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CACA 360

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Db 301

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CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCACTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

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Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAAGATAGAGATTCCCCT-

GGACCACACCTCCGTGGTTC 1559

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Db 1501

AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTG
GTTC 1560

Qy 1560

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1619

|||||

Db 1561

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1620

Qy 1620

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1679

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Db 1621

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1680

Qy 1680

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1739

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Db 1681

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1740

Qy 1740

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA
CC 1799

|||||

Db 1741

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAA
CC 1800

Qy 1800

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA
1859

|||||

Db 1801

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA
1860

Qy 1860

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAA 1919

|||||

Db 1861

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAG
AGAA 1920

Qy 1920

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

|||||

Db 1921

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1980

Qy 1980

TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

|||||

Db 1981

TTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 13

AX002655

LOCUS AX002655 2541 bp DNA linear PAT 10-MAR-2000

DEFINITION Sequence 1 from Patent EP0855444.

ACCESSION AX002655

VERSION AX002655.1 GI:7242133

KEYWORDS .

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 2541)

AUTHORS Murphy,K. and Chapman,C.G.

TITLE Aspartic proteinase 2 (ASP2)

JOURNAL Patent: EP 0855444-A 1 29-JUL-1998;

SMITHKLINE BEECHAM PLC (GB); SMITHKLINE BEECHAM CORP (US)

FEATURES Location/Qualifiers

source 1. .2541

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

|||||

Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121

CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181

GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

|||||

Db 781

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

|||||

Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

|||||

Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-
GGACCACACCTCCGTGGTTC 1559

|||||

Db 1501

AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTG
GTTC 1560

Qy 1560

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1619

|||||

Db 1561

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1620

Qy 1620

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1679

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Db 1621

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1680

Qy 1680

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1739

|||||

Db 1681

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1740

Qy 1740

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAA
CC 1799

|||||

Db 1741

TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAA
CC 1800

Qy 1800

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA
1859

|||||

Db 1801

TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA
1860

Qy 1860

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGA
GAA 1919

|||||

Db 1861

AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAG
AGAA 1920

Qy 1920

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

|||||

Db 1921

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1980

Qy 1980

TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

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Db 1981

TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 14

AX700452

LOCUS AX700452 2541 bp DNA linear PAT 03-APR-2003

DEFINITION Sequence 7 from Patent WO03012089.

ACCESSION AX700452

VERSION AX700452.1 GI:29536241

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yon,J., Cleasby,A., Bruinzeel,W.D., Masure,S.L., Tickle,I. and
Sharff,A.

TITLE Crystal structure of beta-site app cleaving enzyme (bace) and use
thereof

JOURNAL Patent: WO 03012089-A 7 13-FEB-2003;

Astex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)

FEATURES Location/Qualifiers

source 1. .2541

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1
ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

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Db 1
ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61
GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

|||||

Db 61
GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

Qy 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

|||||

Db 121
CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGC
AGCTTT 180

Qy 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

|||||

Db 181
GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGA
TGACC 240

Qy 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

Qy 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATC
CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

|||||

Db 541

GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGAC
TCT 600

Qy 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGC
TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

CCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

|||||

Db 661

CCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

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Db 781

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

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Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

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Db 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

Qy 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

|||||||||||||||||||||||||||||||||||||||||

Db 961

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGAA
CATT 1020

Qy 1021

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||||||||||||||||||||||||||||||||||||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

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Db 1081

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGA
CTGT 1140

Qy 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

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Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

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Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

|||||

Db 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGA
CATG 1320

Qy 1321
GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

|||||

Db 1321
GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCC
TAT 1380

Qy 1381
GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

|||||

Db 1381
GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAG
TGG 1440

Qy 1441
CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

|||||

Db 1441
CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTG
CTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-
GGACCACACCTCCGTGGTTC 1559

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Db 1501
AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTG
GTTC 1560

Qy 1560
ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1619

|||||

Db 1561

ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGAC
CCTC 1620

Qy 1620

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1679

|||||

Db 1621

CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGT
TCCA 1680

Qy 1680

GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGA
ATAC 1739

|||||

Db 1681

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Qy 1740

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Qy 1800

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Db 1861
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Qy 1920
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TAT 1979

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Db 1921
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TAT 1980

Qy 1980
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Db 1981
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TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 15

E50816

LOCUS E50816 2541 bp DNA linear PAT 18-JUN-2001

DEFINITION Aspartate proteinase ASP2.

ACCESSION E50816

VERSION E50816.1 GI:13023199

KEYWORDS JP 2000060579-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 2541)

AUTHORS David,J.P., Conrad,G.C., Kay,M. and Trudy,S.S.

TITLE Aspartate proteinase ASP2

JOURNAL Patent: JP 2000060579-A 1 29-FEB-2000;

SMITHKLINE BEECHAM CORP

COMMENT OS Unidentified

PN JP 2000060579-A/1

PD 29-FEB-2000

PF 03-AUG-1999 JP 1999219665

PR 28-JAN-1997 GB 9701684:4

PI DAVID J POWERU,CONRAD G CHAPPUMAN,KAY MAFI,TRUDY S SMITH

PC

C12N15/09,A61K31/7088,A61K38/46,A61K39/00,A61K39/395, PC

A61K39/395,A61K48/00,

PC A61P25/28,A61P35/00,A61P43/00,C07K16/40,C12N1/15,C12N1/19, PC

C12N1/21,

PC C12N5/10,C12N9/64,C12Q1/37,G01N33/15,G01N33/50,G01N33/53, PC

G01N33/566,

PC G01N33/577//C12P21/08,C12N15/00,A61K37/54,C12N5/00 CC

Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1. .2541

FT /organism='Unidentified'.

FEATURES Location/Qualifiers

source 1. .2541

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

BASE COUNT 598 a 673 c 675 g 579 t 16 others

ORIGIN

Query Match 98.2%; Score 2032; DB 6; Length 2541;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

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Db 1

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTG
CCCAC 60

Qy 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
CTGGGG 120

|||||

Db 61

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCC
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Qy 121

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|||||

Db 121

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Qy 181

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TGACC 240

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Db 181

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TGACC 240

Qy 241

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TGCA 300

|||||

Db 241

GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTT
TGCA 300

Qy 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

|||||

Db 301

GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAG
CACA 360

Qy 361

TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGG
GGAG 420

|||||

Db 361

TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAG
GGGAG 420

Qy 421

CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAA
CATT 480

|||||

Db 421

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CATT 480

Qy 481

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CTG 540

|||||

Db 481

GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATC
CTG 540

Qy 541

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|||||

Db 541

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TCT 600

Qy 601

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TTC 660

|||||

Db 601

CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGC
TTC 660

Qy 661

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TATC 720

|||||

Db 661

CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGG
TATC 720

Qy 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

|||||

Db 721

GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTA
TTAT 780

Qy 781

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GGAG 840

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Db 781

GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAA
GGAG 840

Qy 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
AAA 900

|||||

Db 841

TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAG
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Qy 901

GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCT
GAT 960

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Db 901

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Qy 961

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Db 961

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Qy 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

|||||

Db 1021

TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCA
CC 1080

Qy 1081

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CTGT 1140

|||||

Db 1081

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CTGT 1140

Qy 1141

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GAG 1200

|||||

Db 1141

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATG
GAG 1200

Qy 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

|||||

Db 1201

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCT
TGC 1260

Qy 1261

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGA
CATG 1320

|||||

Db 1261

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CATG 1320

Qy 1321

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TAT 1380

|||||

Db 1321
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TAT 1380

Qy 1381
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TGG 1440

|||||

Db 1381
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TGG 1440

Qy 1441
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CTG 1500

|||||

Db 1441
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GGACCACACCTCCGTGGTTC 1559

|||||

Db 1501
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GTTC 1560

Qy 1560
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CCTC 1619

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Db 1561
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CCTC 1620

Qy 1620

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TCCA 1679

|||||

Db 1621

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TCCA 1680

Qy 1680

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ATAC 1739

|||||

Db 1681

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ATAC 1740

Qy 1740

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CC 1799

|||||

Db 1741

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Qy 1800

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1859

|||||

Db 1801

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Qy 1860

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GAA 1919

|||||

Db 1861

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AGAA 1920

Qy 1920

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1979

|||||

Db 1921

GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGC
TAT 1980

Qy 1980

TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2039

|||||

Db 1981

TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCT
TG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059

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Db 2041 AATTAAAAAAAAAACTAGA 2060

Search completed: January 21, 2004, 13:29:20

Job time : 7664 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2004, 09:01:24 ; Search time 579 Seconds
(without alignments)
9650.841 Million cell updates/sec

Title: US-09-869-414A-3
Perfect score: 2070
Sequence: 1 atggcccaagccctgccctg.....aaaaaaaaaaaaaaaaaaaaa 2070

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	2070	100.0	2070	21	AAA15662		Human aspartyl pro
2	2070	100.0	2070	22	AAD17865		Human aspartyl pro
3	2070	100.0	2070	22	AAD13021		Human aspartyl pro
4	2070	100.0	2070	22	AAS11517		Human cDNA encodin
5	2070	100.0	2070	22	AAS11702		DNA encoding human
6	2070	100.0	2070	22	AAD06739		Human aspartyl pro
7	2070	100.0	2070	24	ABL52457		Human Asp-2(a) nuc
8	2070	100.0	2070	24	ABL49914		Human aspartyl pro
9	2047.8	98.9	16080	21	AAA59553		DNA clone pCEK Cl.
10	2039.8	98.5	2348	21	AAA59551		DNA encoding a hum
11	2032	98.2	2541	19	AAV41696		Nucleotide sequenc
12	2010	97.1	3252	22	AAF31848		Human memapsin 2 c
13	2010	97.1	3252	22	AAF28101		Memapsin 2 DNA. H
14	2010	97.1	3252	24	ABK91244		Human cDNA encodin
15	2010	97.1	3252	24	ABK88641		cDNA encoding huma
16	2010	97.1	3252	25	ABX11591		Human partial cDNA
17	1894.2	91.5	5757	24	ABL39774		Human NS cDNA sequ
18	1887.2	91.2	1977	21	AAA15663		Human aspartyl pro
19	1887.2	91.2	1977	22	AAD17866		Human aspartyl pro
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22	1887.2	91.2	1977	22	AAS11703		DNA encoding human
23	1887.2	91.2	1977	22	AAD06740		Human aspartyl pro
24	1887.2	91.2	1977	24	ABL52458		Human Asp-2(b) nuc
25	1887.2	91.2	1977	24	ABL49915		Human aspartyl pro
26	1843.4	89.1	2370	19	AAV41697		Partial nucleotide
27	1788.8	86.4	1979	22	AAK94824		Human full-length
28	1655.8	80.0	1746	25	ACC51071		Human amyloid proc
29	1644.8	79.5	1747	20	AAX97602		Extended human sec
30	1552.4	75.0	2043	21	AAA15664		Murine aspartyl pr
31	1552.4	75.0	2043	22	AAD17867		Murine aspartyl pr
32	1552.4	75.0	2043	22	AAD13023		Murine aspartyl pr
33	1552.4	75.0	2043	22	AAS11519		Mouse cDNA encodin
34	1552.4	75.0	2043	22	AAS11704		DNA encoding mouse
35	1552.4	75.0	2043	22	AAD06741		Murine aspartyl pr
36	1552.4	75.0	2043	24	ABL52459		Mouse Asp-2(a) nuc
c 37	1501.2	72.5	2907	23	AAS82237		DNA encoding novel
38	1499.8	72.5	1503	21	AAA28278		Human cDNA encodin
39	1499.8	72.5	1503	21	AAA59550		DNA encoding a hum
40	1499.8	72.5	1527	24	ABA02406		FLAG-tagged human
41	1487.4	71.9	1911	22	AAD09485		Human aspartyl pro
42	1423	68.7	2914	23	AAS73798		DNA encoding novel
43	1395.4	67.4	2158	24	ABK63758		Rat sequence diffe
44	1359	65.7	1362	21	AAA15688		Modified human asp
45	1359	65.7	1362	22	AAD17878		Human-Asp 2(a) pro

ALIGNMENTS

RESULT 1

AAA15662

ID AAA15662 standard; cDNA; 2070 BP.

XX

AC AAA15662;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human aspartyl protease 2 (a) (Asp2) nucleotide sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

KW Alzheimer's disease; beta secretase site; ss.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX

PD 30-MAR-2000.

XX

FF 23-SEP-1999; 99WO-US20881.

XX

PR 24-SEP-1998; 98US-0101594.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2000-303209/26.

DR P-PSDB; AAY88425.

XX

PT New enzyme designated human aspartase useful in research into

PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -

XX

PS Claim 5; Fig 2; 183pp; English.

XX

CC This sequence represents the human aspartyl protease 2 (Asp2) nucleotide
 CC sequence. The invention relates to a protease (e.g. Asp2) capable of
 CC cleaving the beta secretase site of amyloid precursor protein (APP). The
 CC protease contains a sequence encoding the amino acid sequence DTG and a
 CC sequence encoding DSG or DTG separated by 100-300 amino acids. When
 CC mutated the APP gene causes an autosomal dominant form of Alzheimer's
 CC disease. APP localises to the cell surface membrane and have a single
 CC C-terminal transmembrane domain. Proteolytic processing of APP produces
 CC the amyloid beta protein, which is possibly very important in Alzheimer's
 CC disease. The invention includes a nucleotide sequence encoding the
 CC protease, a vector containing the nucleotide sequence, and a cell line
 CC comprising the vector. Methods for screening for inhibitors of beta
 CC secretase activity are also given in the invention. The human aspartase
 CC protein and nucleotide sequences and the methods for identifying
 CC inhibitors of the protease, are useful in the treatment of and research
 CC in to Alzheimer's disease.

XX

SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match

100.0%; Score 2070; DB 21; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC	60
Qy	61	GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCTGGGGGGCGCCCCCTGGGG	120
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Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
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Qy	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
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Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
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Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGTGGCTTC	660
Qy	661	CCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
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Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
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Qy	1021	TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680

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Qy      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
          |||
Db      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
          |||
Db      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
          |||
Db      1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860

Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
          |||
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
          |||
Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          |||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
          |||
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

```

RESULT 2

AAD17865

ID AAD17865 standard; cDNA; 2070 BP.

XX

AC AAD17865;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human aspartyl protease 2(a) [hu-Asp2(a)] cDNA.

XX

KW Human; aspartyl protease 2(a); Asp2(a); amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;

KW chromosome 11q23.3-24.1; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "Human aspartyl protease 2(a)"

FT sig_peptide 1..63

FT /*tag= b

FT mat_peptide 64..1503

FT /*tag= c

FT /product= "Mature human aspartyl protease 2(a)"

XX

PN GB2357767-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-0023315.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2001-444208/48.
 DR P-PSDB; AAE10629.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 PS Example 2; Fig 2; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 CC Asp1 proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Asp1 alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is a cDNA encoding
 CC long form of human Asp2 protein, designated as Asp2(a). Asp2 gene is
 CC localised on chromosome 11q23.3-24.1.
 XX
 SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

 Query Match 100.0%; Score 2070; DB 22; Length 2070;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCCTGCCCCAC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCCTGCCCCAC 60

 Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020

Db	961	 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Db	1201	 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860

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Db      1801 TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
        |||
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Qy      1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
        |||
Db      1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
        |||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Qy      2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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Db      2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 3

AAD13021

ID AAD13021 standard; cDNA; 2070 BP.

XX

AC AAD13021;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human aspartyl protease 2a (Hu-Asp2a) cDNA.

XX

KW Human; aspartyl protease 2a; Asp 2a; beta-amyloid precursor protein; APP;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
 KW neuroprotective; antisense therapy; gene therapy;
 KW chromosome 11q23.3-24.1; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "Human aspartyl protease 2a (Hu-Asp2a)"

FT sig_peptide 1..63

FT /*tag= b

FT mat_peptide 64..1503

FT /*tag= c

FT /product= "Mature human aspartyl protease 2a (Hu-Asp2a)"

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB00799.

XX

PR 09-MAY-2001; 2001WO-IB00799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-483072/52.

DR P-PSDB; AAE06859.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -

XX

PS Claim 98; Fig 2; 185pp; English.

XX

CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting
CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC blots. The present cDNA sequence encodes human aspartyl protease 2
CC (Hu-Asp2), a 'long' form designated as (Hu-Asp2a). Hu-Asp 2 gene is
CC localised on chromosome 11q23.3-24.1.

XX

SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Db	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Qy	61	GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240

Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Db	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141		TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141		TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261		CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261		CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501		AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501		AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561		CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561		CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621		CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621		CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681		GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681		GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741		CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1741		CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Qy	1801		TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801		TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861		GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861		GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921		AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

Db 1921 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
 ||||||||||||||||||||||||||||
 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 4

AAS11517

ID AAS11517 standard; cDNA; 2070 BP.

XX

AC AAS11517;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA encoding Aspartyl protease 2(a), Asp2(a).

XX

KW Human; Aspartyl protease; Asp2(a); beta-secretase; nootropic;

KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;

KW amyloid-beta; Abeta; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	1..1506
----	-----	---------

FT		/*tag= a
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FT		/product= "Asp2(a)"
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FT	sig_peptide	1..63
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FT		/*tag= b
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FT	sig_peptide	64..135
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FT		/*tag= c
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FT		/label= Pre_pro_peptide
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FT	sig_peptide	136..171
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FT		/*tag= d
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FT		/label= Pro_peptide
----	--	---------------------

FT	mat_peptide	172..1503
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FT		/*tag= e
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FT		/label= Mature_Asp2(a)
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XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB00798.

XX

PR 09-MAY-2001; 2001WO-IB00798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCC'TGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCC'TGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCC'TGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCC'TGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Qy 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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 Db 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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 Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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 Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
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 Db 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320

Qy 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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 Db 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG 1440
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 Db 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG 1440

Qy 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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 Db 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTGGACCACACCTCCGTGGTTCA 1560
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 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTGGACCACACCTCCGTGGTTCA 1560

Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
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 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740
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 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740

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 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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 Db 1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

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Db      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Qy      2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 ATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 5

AAS11702

ID AAS11702 standard; DNA; 2070 BP.

XX

AC AAS11702;

XX

DT 24-OCT-2001 (first entry)

XX

DE DNA encoding human aspartyl protease 2a (Asp-2a).

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; ds.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	1..1506
----	-----	---------

FT		/*tag= a
----	--	----------

FT		/product= "Aspartyl protease-2a (Asp-2a)"
----	--	---

FT	sig_peptide	1..63
----	-------------	-------

FT		/*tag= b
----	--	----------

FT	misc_feature	64..135
----	--------------	---------

FT		/*tag= c
----	--	----------

FT		/note= "Pre-propeptide"
----	--	-------------------------

FT	misc_feature	136..171
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FT		/*tag= d
----	--	----------

FT		/note= "Propeptide"
----	--	---------------------

FT	mat_peptide	172..1503
----	-------------	-----------

FT		/*tag= e
----	--	----------

FT		/note= "Mature Aspartyl protease-2a"
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XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB00797.

XX

PR 09-MAY-2001; 2001WO-IB00797.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.


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XX      Bienkowski MJ,  Gurney ME,  Heinrikson RL,  Parodi LA,  Yan R;
XX
DR      WPI; 2001-502548/55.
DR      P-PSDB; AAU07102.
XX
PT      Novel purified polypeptide comprising fragment of mammalian aspartyl
PT      protease 2, lacking Asp2 transmembrane domain and retaining beta
PT      secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT      activity -
XX
PS      Claim 98; Fig 2; 185pp; English.
XX
CC      The invention relates to a novel purified polypeptide comprising a
CC      fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC      Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC      and the fragment retain the beta-secretase activity of the mammalian Asp2
CC      protein. Also included is an isoform of amyloid protein precursor (APP)
CC      comprising the amino acid sequence of a APP or its fragment containing
CC      an APP cleavage site recognisable by a mammalian beta-secretase, and
CC      further comprising two lysine residues at the carboxyl terminus of the
CC      amino acid sequence of the mammalian APP or APP fragment. The
CC      polypeptides are used for assaying for modulators of beta-secretase
CC      activity; identifying agents that inhibit the APP processing activity
CC      of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC      modulate the activity of Asp2; and for reducing cellular production of
CC      amyloid beta (Abeta) from APP. Agents identified by the above methods
CC      are useful for treating Alzheimer's disease; and for identifying
CC      modulators of amyloid-beta (Abeta) peptide production, for use in
CC      designing therapeutics for the treatment or prevention of Alzheimer's
CC      disease. Probes and primers derived from Asp nucleic acid sequences
CC      are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC      Northern and Southern blots. The present sequence represents the
CC      coding sequence of human Asp-2a used in the methods of the invention.
XX
SQ      Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match          100.0%;  Score 2070;  DB 22;  Length 2070;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 2070;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGGCAGCTTT 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGGCAGCTTT 180

Qy      181 GTGGAGATGGTGGACAACCTGAGGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GTGGAGATGGTGGACAACCTGAGGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

```

Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Db	1081	 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTTGGACCACACCTCCGTGGTTCA	1560
Db	1501	 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	 GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 |||

Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
 |||

Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 6

AAD06739

ID AAD06739 standard; cDNA; 2070 BP.

XX

AC AAD06739;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human aspartyl protease 2a (Asp2a) cDNA.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp 2a;

KW beta-secretase; chromosome 11q23.3-24.1; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..1506

FT /*tag= a

FT /product= "Human aspartyl protease 2a"

FT sig_peptide 1..63

FT /*tag= b

FT sig_peptide 64..135

FT /*tag= c

FT /note= "Pre-pro-peptide"

FT sig_peptide 136..171

FT /*tag= d

FT /note= "Pro-peptide"

FT mat_peptide 172..1503

FT /*tag= e

FT /product= "Human mature aspartyl protease 2a"

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US26080.

XX

PR 23-SEP-1999; 99US-0155493.

PR 23-SEP-1999; 99WO-US20881.

PR 13-OCT-1999; 99US-0416901.

PR 06-DEC-1999; 99US-0169232.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;

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XX
DR   WPI; 2001-290516/30.
DR   P-PSDB; AAE02581.
XX
PT   Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT   protein, useful for the treatment of Alzheimer's disease -
XX
PS   Example 2; Page 126-127; 189pp; English.
XX
CC   The present invention relates to enzymes for cleaving the alpha-
CC   secretase site of the amyloid precursor protein (APP) and methods of
CC   identifying those enzymes. The methods may be used to identify enzymes
CC   that may be used to cleave the alpha-secretase cleavage site of the APP
CC   protein. The enzymes may be used to treat or modulate the progress of
CC   Alzheimer's disease. The present sequence is human aspartyl protease
CC   (Asp) 2a cDNA. Asp 2a has beta-secretase protease activity. Asp2 gene
CC   is located on chromosome 11q23.3-24.1.
XX
SQ   Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match          100.0%; Score 2070; DB 22; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120
        |||||||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||||||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||||||
Db      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy      241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        |||||||
Db      241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy      301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||||||
Db      301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy      361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||||||
Db      361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy      421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
        |||||||
Db      421 CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy      481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

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Db	481	 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACCTATGACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACCTATGACAAGAGCATTTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380

Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 7

ABL52457

ID ABL52457 standard; cDNA; 2070 BP.

XX

AC ABL52457;

XX

DT 16-JUL-2002 (first entry)
 XX
 DE Human Asp-2(a) nucleotide sequence SEQ ID NO:3.
 XX
 KW Human; Asp-1; Asp-2; aspartyl protease; enzyme; Alzheimer's disease;
 KW proteolytic; chromosome 11q23.3-24.1; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1506
 FT /*tag= a
 FT /product= "Asp-2(a)"
 FT /note= "aspartyl protease"
 XX
 PN GB2367060-A.
 XX
 PD 27-MAR-2002.
 XX
 PF 29-OCT-2001; 2001GB-0025934.
 XX
 PR 23-SEP-1999; 99US-155493P.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-169232P.
 PR 22-SEP-2000; 2000GB-0023315.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2002-396337/43.
 DR P-PSDB; ABB78590.
 XX
 PT Human aspartyl protease 1 substrates useful in assays to detect
 PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 PT disease -
 XX
 PS Example 2; Fig 2; 182pp; English.
 XX
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
 CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain); (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or

Qy	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 8

ABL49914

ID ABL49914 standard; DNA; 2070 BP.

XX

AC ABL49914;

XX

DT 31-MAY-2002 (first entry)

XX

DE Human aspartyl protease nucleotide sequence SEQ ID NO:1.

XX

KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;

KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;

KW Alzheimer's disease; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200206306-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US23035.
 XX
 PR 19-JUL-2000; 2000US-219795P.
 PR 12-MAR-2001; 2001US-275251P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrikson RL;
 XX
 DR WPI; 2002-216995/27.
 DR P-PSDB; ABB06409.
 XX
 PT Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease -
 XX
 PS Claim 1; Page 117; 188pp; English.
 XX
 CC The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful
 CC as a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

Query Match 100.0%; Score 2070; DB 24; Length 2070;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Db	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Qy	61	GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240

Db	181		GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Db	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Qy	301		GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301		GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAAACATT	480
Db	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAAACATT	480
Qy	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541		GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541		GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAAATGGACTGCAAGGAG	840
Db	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAAATGGACTGCAAGGAG	840
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
 ||||||||||||||||||||||||||||
 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 9

AAA59553

ID AAA59553 standard; DNA; 16080 BP.

XX

AC AAA59553;

XX

DT 14-NOV-2000 (first entry)

XX

DE DNA clone pCEK C1.27 encoding a human beta-secretase enzyme.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor; ss.

XX

OS Homo sapiens.

XX

PN WO200047618-A2.

XX

PD 17-AUG-2000.

XX

PF 10-FEB-2000; 2000WO-US03819.

XX

PR 10-FEB-1999; 99US-0119571.

PR 15-JUN-1999; 99US-0139172.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;

XX

DR WPI; 2000-533011/48.

XX

PT Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease -

XX

PS Disclosure; Fig 13A-E; 121pp; English.

XX

CC The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to

CC a mammalian subject e.g. with Alzheimer's disease or Alzheimer's
CC disease-like pathology to test if they maintain or improve cognitive
CC ability or reduce the plaque burden. The compounds are used for the
CC treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
CC present sequence encodes a human beta-secretase enzyme.

XX

SQ Sequence 16080 BP; 3627 A; 4556 C; 3962 G; 3913 T; 22 other;

Query Match 98.9%; Score 2047.8; DB 21; Length 16080;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2052; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
      |||
Db    1675 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 1734

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      |||
Db    1735 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 1794

Qy     121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180
      |||
Db    1795 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 1854

Qy     181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      |||
Db    1855 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 1914

Qy     241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
      |||
Db    1915 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 1974

Qy     301 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      |||
Db    1975 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 2034

Qy     361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      |||
Db    2035 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 2094

Qy     421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
      |||
Db    2095 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 2154

Qy     481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
      |||
Db    2155 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 2214

Qy     541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
      |||
Db    2215 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 2274

Qy     601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
      |||
Db    2275 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 2334

Qy     661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
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Db	2335		CCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC	2394
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	2395		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	2454
Qy	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	2455		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	2514
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Db	2515		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	2574
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	2575		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	2634
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	2635		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	2694
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	2695		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	2754
Qy	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	2755		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	2814
Qy	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	2815		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	2874
Qy	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	2875		GCCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	2934
Qy	1261		CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	2935		CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	2994
Qy	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	2995		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	3054
Qy	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	3055		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	3114
Qy	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	3115		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	3174
Qy	1501		AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCCTGGACCACACCTCCGTGGTTCA	1560

Db	3175	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTC	3234
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Db	3235	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	3294
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	3295	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	3354
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	3355	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	3414
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	3415	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	3474
Qy	1801	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	3475	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	3534
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	3535	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	3594
Qy	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	3595	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	3654
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	3655	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	3714
Qy	2041	ATTAAAAAAAAAAAAAAAAA	2059
Db	3715	ATTAAAAAAAAAACTAGA	3733

RESULT 10

AAA59551

ID AAA59551 standard; DNA; 2348 BP.

XX

AC AAA59551;

XX

DT 14-NOV-2000 (first entry)

XX

DE DNA encoding a human beta-secretase enzyme.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW inhibitor; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 306..1811

Db	486	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	545
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	546	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	605
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	606	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	665
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	666	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	725
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	726	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	785
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	786	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	845
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	846	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	905
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	906	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	965
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	966	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	1025
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	1026	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	1085
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	1086	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	1145
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	1146	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	1205
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	1206	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	1265
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	1266	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1325
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1326	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1385

Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1386	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1445
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1446	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1505
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1506	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1565
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1566	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1625
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1626	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1685
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Db	1686	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1745
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1746	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1805
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1806	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1865
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Db	1866	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1925
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1926	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1985
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1986	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	2045
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	2046	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	2105
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	2106	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	2165
Qy	1861	GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	2166	GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	2225

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 |||
 Db 2226 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 2285

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 |||
 Db 2286 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2345

Qy 2041 ATT 2043
 |||
 Db 2346 ATT 2348

RESULT 11

AAV41696

ID AAV41696 standard; cDNA; 2541 BP.

XX

AC AAV41696;

XX

DT 26-OCT-1998 (first entry)

XX

DE Nucleotide sequence of human ASP2 (aspartic protease 2).

XX

KW Human; ASP2; aspartic protease 2; agonist; antagonist; immunospecific;
 KW antibody; inhibition; Alzheimer's disease; cancer; proteinase;
 KW prohormone processing; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	1..1506
FT		/*tag= a
FT		/product= "human ASP2"

XX

PN EP855444-A2.

XX

PD 29-JUL-1998.

XX

PF 27-JAN-1998; 98EP-0300573.

XX

PR 28-JAN-1997; 97GB-0001684.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Chapman CG, Murphy K, Powell DJ, Smith TS;

XX

DR WPI; 1998-389809/34.

DR P-PSDB; AAW59807.

XX

PT New nucleic acid encoding human aspartic protease 2 - used to treat,
 PT prevent and diagnose e.g. Alzheimer's disease, cancer and prohormone
 PT processing

XX

PS Claim 2; Pages 6-7; 26pp; English.

XX

CC This is the nucleotide sequence of the human ASP2 (aspartic protease 2),

CC used in the method of the invention. Agonists and antagonists for
CC ASP2 immunospecific antibodies are used to treat conditions requiring
CC increased or decreased activity or expression of ASP2 respectively.
CC ASP2 is used to treat and diagnose e.g. Alzheimer's disease, cancer
CC and prohormone processing and ASP2 or a fragment can be used to induce
CC an immune response against the above conditions.

XX

SQ Sequence 2541 BP; 598 A; 673 C; 675 G; 579 T; 16 other;

Query Match 98.2%; Score 2032; DB 19; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        |||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT 480
        |||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG 540
        |||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        |||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
        |||
Db    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660
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Qy	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTC	1559

PD 04-JAN-2001.
 XX
 PF 27-JUN-2000; 2000WO-US17742.
 XX
 PR 28-JUN-1999; 99US-0141363.
 PR 30-NOV-1999; 99US-0168060.
 PR 25-JAN-2000; 2000US-0177836.
 PR 27-JAN-2000; 2000US-0178368.
 PR 08-JUN-2000; 2000US-0210292.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (UNII) UNIV ILLINOIS FOUND.
 XX
 PI Tang JJN, Hong L, Ghosh AK;
 XX
 DR WPI; 2001-137933/14.
 DR P-PSDB; AAB66572.
 XX
 PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2
 PT having 2 catalytic aspartic residues and substrate binding cleft, used
 PT to treat Alzheimer's disease by blocking amyloid precursor protein
 PT cleavage -
 XX
 PS Example 1; Page 70-71; 86pp; English.
 XX
 CC The present sequence is given in a specification relating to an inhibitor
 CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
 CC active site, which is defined by the presence of two catalytic aspartic
 CC residues and a substrate binding cleft. The inhibitor is useful for
 CC the treatment and diagnosis of Alzheimer's disease. It is useful in
 CC screens for individuals with a genetic predisposition to Alzheimer's
 CC disease. The inhibitor is useful as a reagent for specifically binding to
 CC memapsin 2 or memapsin 2 analogues and for aiding in memapsin 2
 CC isolation, purification and characterisation.
 XX
 SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 22; Length 3252;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	40	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGC	99
Db	1	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGC	60
Qy	100	CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG	159
Db	61	CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG	120
Qy	160	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	219
Db	121	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240

Qy 280 ACAGGCAGCAGTAAC TTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC 339
 |||

Db 241 ACAGGCAGCAGTAAC TTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC 300

Qy 340 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
 |||

Db 301 CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy 400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC 459
 |||

Db 361 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC 420

Qy 460 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
 |||

Db 421 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 480

Qy 520 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
 |||

Db 481 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 540

Qy 580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639
 |||

Db 541 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 600

Qy 640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG 699
 ||

Db 601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG 660

Qy 700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
 |||

Db 661 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 720

Qy 760 ATCCGGCGGGAGTGGTATTATGAGGTATCATTGTGCGGGTGGAGATCAATGGACAGGAT 819
 |||

Db 721 ATCCGGCGGGAGTGGTATTATGAGGTATCATTGTGCGGGTGGAGATCAATGGACAGGAT 780

Qy 820 CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC 879
 |||

Db 781 CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC 840

Qy 880 AACCTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 939
 |||

Db 841 AACCTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC 900

Qy 940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 999
 |||

Db 901 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA 960

Qy 1000 GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1059
 |||

Db 961 GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC 1020

Qy 1060 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1119
 |||

Db 1021 AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1080

Qy 1120 GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT 1179

Db	1081		GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180		ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141		ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240		GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201		GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300		CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261		CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360		ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321		ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420		TGCCTCATGGTGTGTCACTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381		TGCCTCATGGTGTGTCACTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480		GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441		GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540		GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501		GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600		CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561		CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660		GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621		GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720		CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681		CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780		TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741		TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840		CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1899
Db	1801		CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1860
Qy	1900		TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1959
Db	1861		TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1920
Qy	1960		GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT	2019

Db 1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy 2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAAAAA 2057
 |||||

Db 1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAACCTAGA 2018

RESULT 13

AAF28101

ID AAF28101 standard; DNA; 3252 BP.

XX

AC AAF28101;

XX

DT 02-APR-2001 (first entry)

XX

DE Memapsin 2 DNA.

XX

KW Memapsin 2; catalyst; Alzheimer's; ds.

XX

OS Homo sapiens.

XX

PN WO200100663-A2.

XX

PD 04-JAN-2001.

XX

PF 27-JUN-2000; 2000WO-US17661.

XX

PR 28-JUN-1999; 99US-0141363.

PR 30-NOV-1999; 99US-0168060.

PR 25-JAN-2000; 2000US-0177836.

PR 27-JAN-2000; 2000US-0178368.

PR 08-JUN-2000; 2000US-0210292.

XX

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX

PI Tang JJN, Lin X, Koelsch G;

XX

DR WPI; 2001-102885/11.

XX

PT Purified recombinant catalytically active memapsin 2, used to screen
 PT inhibitors of it, which are used to treat and prevent Alzheimer's
 PT disease -

XX

PS Example 1; Page 71-72; 86pp; English.

XX

CC The present invention relates to a purified recombinant
 CC catalytically active memapsin 2. The invention may be used for
 CC isolating inhibitors which are used to treat or prevent
 CC Alzheimer's disease. The invention may also be used to screen
 CC for individuals more genetically prone to develop Alzheimer's
 CC disease.

XX

SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 22; Length 3252;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	40	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	99
Db	1	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	60
Qy	100	CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG	159
Db	61	CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG	120
Qy	160	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	219
Db	121	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	420
Qy	460	GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCA ACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	TCCA ACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTATCATTTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTATCATTTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840

Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTCACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTCACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCC'CTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779

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Db      1681  CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1740
Qy      1780  TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT 1839
Db      1741  TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT 1800
Qy      1840  CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899
Db      1801  CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1860
Qy      1900  TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
Db      1861  TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920
Qy      1960  GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
Db      1921  GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980
Qy      2020  GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
Db      1981  GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 14

ABK91244

ID ABK91244 standard; cDNA; 3252 BP.

XX

AC ABK91244;

XX

DT 15-NOV-2002 (first entry)

XX

DE Human cDNA encoding Memapsin 2.

XX

KW Human; ss; gene; memapsin 2; aspartic protease; beta secretase;
KW degenerative disease; Alzheimer's disease; amyloid precursor protein;
KW APP; neuroprotective; nootropic; inhibitor;
KW substrate side-chain preference.

XX

OS Homo sapiens.

XX

PN WO200253594-A2.

XX

PD 11-JUL-2002.

XX

PF 28-DEC-2001; 2001WO-US50826.

XX

PR 28-DEC-2000; 2000US-258705P.

PR 14-MAR-2001; 2001US-275756P.

XX

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA (UNII) UNIV ILLINOIS FOUND.

XX

PI Tang JJN, Koelsch G, Ghosh AK;

XX

DR WPI; 2002-619088/66.

DR P-PSDB; ABG78372, ABG78374.

XX
PT New memapsin 2 activity inhibitor useful in treatment of e.g.
PT Alzheimer's disease -
XX
PS Disclosure; Fig 6; 74pp; English.
XX
CC The invention relates to an inhibitor of catalytically active memapsin 2
CC (an aspartic protease which can cleave at beta secretase sites), which
CC binds to the active site of memapsin 2 defined by the presence of two
CC catalytic aspartic residues and substrate binding cleft. Also
CC included is a method of determination of the substrate side-chain
CC preference in memapsin 2 sub-sites comprising: (a) reacting a mixture of
CC memapsin 2 substrates with memapsin 2, and determining the sub-site
CC preference of memapsin 2 by determining relative initial hydrolysis rates
CC of the mixture of memapsin 2 substrates; or (b) preparing a combinatorial
CC library of memapsin 2 inhibitors containing a base sequence taken from
CC OM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of
CC inhibitors with memapsin 2 which binds to several inhibitors to generate
CC several bound memapsin 2, and detecting the bound memapsin 2 with an
CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
CC secondary antibody. The inhibitors may be used in the manufacture of a
CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
CC be involved in the cleavage of amyloid precursor protein (APP), and for
CC determining the substrate side-chain preference in memapsin 2 sub-sites.
CC The present sequence encodes human memapsin 2.
XX
SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 24; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	40	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	99
Db	1	GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC	60
Qy	100	CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG	159
Db	61	CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG	120
Qy	160	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	219
Db	121	CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459

Db	361		CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	420
Qy	460		GTCACGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421		GTCACGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520		TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481		TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580		CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541		CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640		CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG	699
Db	601		CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG	660
Qy	700		AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661		AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760		ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721		ATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820		CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781		CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880		AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841		AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940		TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901		TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000		GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961		GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060		AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021		AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120		GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081		GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180		ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141		ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240		GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTTACGGACGGCAGCGGTGGAAGGC	1299

Db	1201	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
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Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
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Db	1501	GGACCACACCTCCGTGGTTCACCTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATT	1800
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Db	1861	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1920
Qy	1960	GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT	2019
Db	1921	GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT	1980
Qy	2020	GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA	2057
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ID ABK88641 standard; cDNA; 3252 BP.
XX
AC ABK88641;
XX
DT 07-OCT-2002 (first entry)
XX
DE cDNA encoding human memapsin 2.
XX
KW Human; memapsin 2; beta secretase; aspartic protease; APP;
KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
KW neuroprotective; nootropic; expressed sequence tag; EST; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1467
FT /*tag= a
FT /partial
FT /product= "Memapsin 2"
FT /note= "This sequence lacks a start codon"
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PN US2002049303-A1.
XX
PD 25-APR-2002.
XX
PF 28-FEB-2001; 2001US-0796264.
XX
PR 28-JUN-1999; 99US-141363P.
PR 30-NOV-1999; 99US-168060P.
PR 25-JAN-2000; 2000US-177836P.
PR 27-JAN-2000; 2000US-178368P.
PR 27-JUN-2000; 2000US-0604608.
XX
PA (TANG/) TANG J J N.
PA (LINX/) LIN X.
PA (KOEL/) KOELSCH G.
PA (HONG/) HONG L.
XX
PI Tang JJN, Lin X, Koelsch G, Hong L;
XX
DR WPI; 2002-507280/54.
DR P-PSDB; AAU99488.
XX
PT New recombinant catalytically active memapsin 2, useful to screen for
PT inhibitors of memapsin 2 which can be used to prevent and treat
PT Alzheimer's disease -
XX
PS Example 1; Page 20-21; 44pp; English.
XX
CC The present invention relates to methods for the production of
CC purified, recombinant catalytically active, memapsin 2 (beta
CC secretase). Memapsin 2, a member of the aspartic protease family,
CC cleaves beta-amyloid precursor protein (APP) found in amyloid plaques.
CC The recombinant memapsin 2 is useful for identifying inhibitors of
CC memapsin 2 in the design of drugs for the treatment and/or prevention
CC of Alzheimer's disease. The recombinant memapsin 2 can be used to
CC immunise against Alzheimer's disease. The present sequence encodes

CC human memapsin 2.

XX

SQ Sequence 3252 BP; 804 A; 863 C; 811 G; 771 T; 3 other;

Query Match 97.1%; Score 2010; DB 24; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy     160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
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Db    121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy     220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
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Db    181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

Qy     280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTAC 339
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Qy     340 CAGAGGCAGCTGTCCAGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399
      |||
Db    301 CAGAGGCAGCTGTCCAGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 360

Qy     400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC 459
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Qy     460 GTCACGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC 519
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Qy     640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG 699
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Db    601 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG 660

Qy     700 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC 759
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

US-09-548-372D-3

; Sequence 3, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-3

Query Match 99.9%; Score 2068.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGACGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTGACGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
 |||
 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 |||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 |||
 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740
 |||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
 |||
 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
 |||
 Db 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 |||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 |||
 Db 1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAIAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAIAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 2

US-09-548-367D-3

; Sequence 3, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 2070
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-548-367D-3

Query Match 99.9%; Score 2068.4; DB 4; Length 2070;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC	60
Db	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC	60
Qy	61	GGCACCAGCAGCGCATCCGGCTGCCCCGCGCAGCGGCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCAGCAGCGCATCCGGCTGCCCCGCGCAGCGGCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660

Db	601		CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	660
Qy	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTCGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781		GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841		TACAACATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841		TACAACATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081		ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141		TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201		GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261		CATGTGCACGATGAGTTTCTAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261		CATGTGCACGATGAGTTTCTAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321		GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381		GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441		CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500

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Db      1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
Qy      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
        |||
Db      1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
Qy      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCTCC 1620
        |||
Db      1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCTCC 1620
Qy      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
        |||
Db      1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
Qy      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
        |||
Db      1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
Qy      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
        |||
Db      1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
Qy      1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
        |||
Db      1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
Qy      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
        |||
Db      1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
Qy      1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
        |||
Db      1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
Qy      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
        |||
Db      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
        |||
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 3

US-09-551-853D-3

; Sequence 3, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-3
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Query Match          99.9%; Score 2068.4; DB 4; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACGTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACGTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440

Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 4

US-09-009-191-1

; Sequence 1, Application US/09009191

; Patent No. 6319689

; GENERAL INFORMATION:

; APPLICANT: POWELL, DAVID

; APPLICANT: CHAPMAN, CONRAD

; APPLICANT: MURPHY, KAY

; APPLICANT: SMITH, TRUDI

; TITLE OF INVENTION: ASP2

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,191
; FILING DATE: 20-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9701684.4
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-191-1

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Query Match          98.2%; Score 2032; DB 4; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy      241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Qy	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTC	1559
Db	1501	AAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTC	1560
Qy	1560	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1619
Db	1561	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1620
Qy	1620	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1679
Db	1621	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1680
Qy	1680	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1739
Db	1681	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1740
Qy	1740	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC	1799
Db	1741	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC	1800
Qy	1800	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1859
Db	1801	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1860
Qy	1860	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCTTGGCAGAGAA	1919
Db	1861	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA	1920
Qy	1920	GAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1979
Db	1921	GAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1980

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Qy      1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
          |||
Db      1981 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040

Qy      2040 AATTAAAAAAAAAAAAAAAAAAAA 2059
          |||
Db      2041 AATTAAAAAAAAAAAACTAGA 2060

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RESULT 5

US-09-604-608-1

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; Sequence 1, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-608-1

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Query Match          97.1%; Score 2010; DB 4; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      40 GCGGGAGTGCTGCCTGCCACGGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGC 99
          |||
Db      1  GCGGGAGTGCTGCCTGCCACGGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGC 60

Qy     100 CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
          |||
Db      61 CTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy     160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGGCAAGTCGGGGCAG 219
          |||
Db     121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGGCAAGTCGGGGCAG 180

Qy     220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279

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Db	181	 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAAC TTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	 ACAGGCAGCAGTAAC TTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATAACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	 CAGAGGCAGCTGTCCAGCACATAACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459
Db	361	 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	420
Qy	460	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	 GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	 TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG	699
Db	601	 CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	 AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	 ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	 CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	 AACCTTCGTTTGCCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	 GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119

Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTGACGCGTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTGACGCGTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTCACTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTCACTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACCTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACCTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA	1959
Db	1861	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA	1920


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Qy      1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
          |||
Db      1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
          |||
Db      1981 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 6

US-09-548-372D-5

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; Sequence 5, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-372D-5

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Query Match          91.2%; Score 1887.2; DB 4; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
          |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
          |||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
          |||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
          |||
Db      181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

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Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568	-----CTTTGTGGTGCTGGCTTC	585
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781	GAGGTCAATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCAACCTTCGTTTGCCCAAGAAA	900
Db	766	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCAACCTTCGTTTGCCCAAGAAA	825
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	826	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	885
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCCTCCGCATCACC	1080
Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCCTCCGCATCACC	1005

Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1785
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1786	GTA CTGGCATCACACGCAGGTTACCTTGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1845
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

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          |||
Db      1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905
Qy      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          |||
Db      1906 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965
Qy      2041 ATTAAAAAAAAA 2052
          | |||
Db      1966 AAAAAAAAAA 1977

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RESULT 7

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US-09-548-367D-5
; Sequence 5, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-5

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Query Match          91.2%; Score 1887.2; DB 4; Length 1977;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
          |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
          |||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180
          |||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180
Qy      181 CTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

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Db	181		GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241		GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301		GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301		GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361		TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421		CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481		GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541		GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541		GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601		CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568		-----CTTTGTGGTGCTGGCTTC	585
Qy	661		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586		CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646		GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781		GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706		GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	766		TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	825
Qy	901		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	826		GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	885
Qy	961		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886		GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945
Qy	1021		TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1005
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTGAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTGAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCAC'TCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCAC'TCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1785
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1786	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1845

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Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
          |||
Db      1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          |||
Db      1906 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965

Qy      2041 ATTAAAAAAAAA 2052
          | |||
Db      1966 AAAAAAAAAA 1977

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RESULT 8

US-09-551-853D-5

; Sequence 5, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 1977

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-551-853D-5

Query Match 91.2%; Score 1887.2; DB 4; Length 1977;

Best Local Similarity 96.2%; Pred. No. 0;

Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

```

Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
          |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
          |||
Db      61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180
          |||
Db      121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCGGAGGGGCAGCTTT 180

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Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568	-----CTTTGTGGTGCTGGCTTC	585
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTTCGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTTCGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	900
Db	766	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA	825
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	826	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	885
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945

Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1005
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCTAGTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCTAGTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCTTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1785
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920

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          |||
Db      1786 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1845

Qy      1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
          |||
Db      1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy      1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          |||
Db      1906 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965

Qy      2041 ATTAIAAAAAAAAA 2052
          | |||
Db      1966 AAAAAAAAAAAAAA 1977

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RESULT 9

US-09-009-191-3

; Sequence 3, Application US/09009191

; Patent No. 6319689

; GENERAL INFORMATION:

; APPLICANT: POWELL, DAVID

; APPLICANT: CHAPMAN, CONRAD

; APPLICANT: MURPHY, KAY

; APPLICANT: SMITH, TRUDI

; TITLE OF INVENTION: ASP2

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/009,191

; FILING DATE: 20-JAN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: UK 9701684.4

; FILING DATE: 28-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70368

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2370 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-009-191-3

Query Match 89.1%; Score 1843.4; DB 4; Length 2370;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1867; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

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Qy      172 GGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTG 231
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Db       1  GGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTG 60

Qy      232 GAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGT 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGT 120

Qy      292 AACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTG 180

Qy      352 TCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGG 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGG 240

Qy      412 GAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACCTGTGCGT 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACCTGTGCGT 300

Qy      472 GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAA 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAA 360

Qy      532 GGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCCTGACGACTCCCTGGAGCCTTTC 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCCTGACGACTCCCTGGAGCCTTTC 420

Qy      592 TTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGT 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 TTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGT 480

Qy      652 GCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATT 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATT 540

Qy      712 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 771
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Db      541 GGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAG 600

Qy      772 TGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 660

Qy      832 TGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTG 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTG 720
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Qy	892	CCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCTCCACGGAGAAG	951
Db	721	CCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCTCCACGGGAGAAG	780
Qy	952	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT	1011
Db	781	TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCT	840
Qy	1012	TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC	1071
Db	841	TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTC	900
Qy	1072	CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA	1131
Db	901	CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA	960
Qy	1132	GACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTT	1191
Db	961	GACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTT	1020
Qy	1192	ATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTC	1251
Db	1021	ATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTC	1080
Qy	1252	AGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCAAC	1311
Db	1081	AGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCAAC	1140
Qy	1312	TTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACC	1371
Db	1141	TTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACC	1200
Qy	1372	ATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTG	1431
Db	1201	ATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTG	1260
Qy	1432	TGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATC	1491
Db	1261	TGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGACAATGGATGACTTTGCTGATGACATC	1320
Qy	1492	TCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCT	1550
Db	1321	TCCCTGCTGAAGTGAGGAGGCCCATGGGAGAAAGATAGAGATTCCCCTGGGACCACACCT	1380
Qy	1551	CCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTC	1610
Db	1381	CCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTC	1440
Qy	1611	AGGACCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGG	1670
Db	1441	AGGACCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGG	1500
Qy	1671	TGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGG	1730
Db	1501	TGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGG	1560

Qy 1731 CGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAG 1790
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 Db 1561 CGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAG 1620
 Qy 1791 CCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTT 1850
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 Db 1621 CCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTT 1680
 Qy 1851 AGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCT 1910
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 Db 1681 AGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCG 1740
 Qy 1911 GGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACA 1970
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 Db 1741 GGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACA 1800
 Qy 1971 GTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGAT 2030
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 Db 1801 GTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGAT 1860
 Qy 2031 TGCCTCTTGAATTAAAAAAAAAAAAAAAAAA 2059
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 Db 1861 TGCCTCTTGAATTAAAAAAAAAAACTAGA 1889

RESULT 10

US-09-548-372D-7

; Sequence 7, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 2043

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-548-372D-7

Query Match 75.0%; Score 1552.4; DB 4; Length 2043;
 Best Local Similarity 87.6%; Pred. No. 0;
 Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCCTGCCAC 60
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 Db 1 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCAG 60

Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
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 Db 61 GGAACCCATCTCGGCATCCGGCTGCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 120

Qy 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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 Db 121 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 180

Qy 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
 ||||| ||||| ||||| ||||| ||||| || || ||||| ||||| ||||| |||||
 Db 181 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 240

Qy 241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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 Db 241 GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACTTTGCA 300

Qy 301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
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 Db 301 GTGGGGGCTGCCCCACACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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 Db 361 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA 420

Qy 421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
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 Db 421 CTGGGCACCGACCTGGTGAACATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy 481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
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 Db 481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAAGTGGGAGGGCATCCTA 540

Qy 541 GGGCTGGCCTATGCTGAGATTGCCAGGCCCTGACGACTCCCTGGAGCCTTCTTTGACTCT 600
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 Db 541 GGGCTGGCCTATGCTGAGATTGCCAGGCCCGACGACTCTTTGGAGCCTTCTTTGACTCC 600

Qy 601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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 Db 601 CTGGTGAAGCAGACCCACATTCCTCAACATCTTTCCCTGCAGCTCTGTGGCGCTGGCTTC 660

Qy 661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
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 Db 661 CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC 720

Qy 721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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 Db 721 GACCACTCGCTATACACGGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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 Db 781 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 840

Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Db	841	TACAACCTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	901	GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCTGGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT	1020
Qy	1021	TTCCCAAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCTCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTATCATGGAA	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGTTTCTATGTCTCTTCGATCGAGCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCGGCAGTGGAAGGTCCGTTTGTACGGCAGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTG	1440
Db	1381	GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAAGTG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCTTGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCTTGACCACATCTGGGTGGTTCC	1560
Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1561	CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	1620
Qy	1619	CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCC	1678
Db	1621	CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC	1679
Qy	1679	AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA	1738

Db 1680 AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739

Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
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Db 1740 TCCTTAGGCACCACAAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798

Qy 1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
 || || ||| || ||||| | ||||| ||||| ||||| | || || |||

Db 1799 CTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854

Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
 ||||| ||| || ||| ||| ||| ||||| ||||| ||||| ||||| |||

Db 1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913

Qy 1919 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
 | | ||| | | ||||| ||||| || ||| | || ||||| |

Db 1914 AAGGGCCAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970

Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
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Db 1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029

Qy 2039 GAATTAATAAAAAAAAA 2052
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Db 2030 GAGATAAACAAGAA 2043

RESULT 11

US-09-548-367D-7

; Sequence 7, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 2043

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-548-367D-7

Query Match 75.0%; Score 1552.4; DB 4; Length 2043;
 Best Local Similarity 87.6%; Pred. No. 0;

Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        ||||| ||| ||| ||||| ||||| ||| ||| ||||| |||||
Db      1 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGAATGCTGCCTGCCCAG 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        || ||||| | ||||| ||||| ||||| ||||| ||| | |||||
Db     61 GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        ||| ||||| ||||| ||||| || | ||||| ||||| |||||
Db    121 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||| ||||| ||||| ||||| ||| ||| ||||| |||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        || ||||| ||||| ||||| ||||| ||||| || ||||| |||||
Db    241 GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 GTGGGGGCTGCCCCACACCCTTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    421 CTGGGCACCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
        ||||| ||||| ||||| ||||| ||||| || ||||| |||||
Db    481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAAGTGGGAGGGCATCCTA 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCCCGACGACTCTTTGGAGCCTTCTTTGACTCC 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db    601 CTGGTGAAGCAGACCCACATTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
        ||||| ||||| | || | ||||| || ||||| ||||| |||||
Db    661 CCCCTCAACCAGACCGAGGCAGTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    721 GACCACTCGCTATACACGGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy    781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db    781 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG 840
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Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTCGCTGTCTCACAGTCATCCACGGGCACTGTTATGGGAGCCGTCATCATGGAA	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCGAAAACGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Db	1201	GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAAGCGAATTGGCTTTGCTGTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCGGCACTGGAAGGTCCGTTTGTTACGGCAGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCGCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCCCTGGACCACATCTGGGTGGTTCC	1560
Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1561	CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	1620
Qy	1619	CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC	1678
Db	1621	CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC	1679

Qy 1679 AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA 1738
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 Db 1680 AGGGCTTGACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739
 Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAAC 1798
 ||| | |||| |||| || || || ||||| ||||| ||||| ||||| ||||| |
 Db 1740 TCCTTAGGCACCACAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798
 Qy 1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
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 Db 1799 CTCTGCCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854
 Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
 ||||| ||| || || |||| ||| ||||| ||||| ||||| ||||| |||||
 Db 1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913
 Qy 1919 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
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 Db 1914 AAGGGCCAATC-TCATTCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970
 Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
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 Db 1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029
 Qy 2039 GAATTAATAAAAAAAAA 2052
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 Db 2030 GAGATAAACAAGAA 2043

RESULT 12

US-09-551-853D-7

; Sequence 7, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 2043

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-551-853D-7

Query Match 75.0%; Score 1552.4; DB 4; Length 2043;
Best Local Similarity 87.6%; Pred. No. 0;
Matches 1800; Conservative 0; Mismatches 241; Indels 13; Gaps 9;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
      ||||| ||| ||| ||||| ||||| ||| ||||| ||||| ||||| |||||
Db      1 ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCCAG 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      || ||||| | ||||| ||||| ||||| ||||| ||| | |||||
Db     61 GGAACCCATCTCGGCATCCGGCTGCCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
      ||| ||||| ||||| ||||| ||| | ||||| ||||| |||||
Db    121 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      ||||| ||||| ||||| ||||| ||| || ||||| ||||| |||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
      || ||||| ||||| ||||| ||||| ||||| ||| ||||| |||||
Db    241 GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 GTGGGGGCTGCCCCACACCCTTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    421 CTGGGCACCGACCTGGTGAAGCATCCCTCATGGCCCCAACGTCACCTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAAGTGGGAGGGGCATCCTA 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCCCGACGACTCTTGGAGCCCTTCTTTGACTCC 600

Qy    601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    601 CTGGTGAAGCAGACCCACATTCCTCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGGAGCATGATCATTGGAGGTATC 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    661 CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    721 GACCACTCGCTATACAGGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy    781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
```

Db	781	GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCCGGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCAGTGTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTGCGTGTCTCACAGTCATCCACGGGCAGTGTATGGGAGCCGTCATCATGGAA	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGTTTCTATGTCGTCTTCGATCGAGCCCCGAAAGCGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCGGCAGTGGGAAGGTCCGTTTGTTACGGCAGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACACTTATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTAGTGG	1440
Db	1381	GTCATGGCGGCCATCTGCGCCCTCTTCATGTTGCCACTCTGCCTCATGGTATGTAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTGCGTTGCCTGCGCCACCAGCACGATGACTTTGCTGATGACATCTCCCTGCTC	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCTGGACCACATCTGGGTGGTTCC	1560
Qy	1561	CTTTGGTCACA--AGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCT	1618
Db	1561	CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCT	1620
Qy	1619	CCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTC	1678

Db 1621 CACCAACCTGCCAATGCTTCTGGCGTGACAGA-ACAGAGAAATCAGGCAAGCTGGATTAC 1679
 Qy 1679 AGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATA 1738
 ||| | | ||||| ||| | | ||| ||| ||| ||| ||| ||| |||
 Db 1680 AGGGCTTGCACCTGTAGGACACAGGAGAGGGAAGGAAGCAGCGTTCTGGTGGCAGGAATA 1739
 Qy 1739 CTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAAC 1798
 ||| | ||| ||| | ||| ||||| ||||| ||||| ||||| |||
 Db 1740 TCCTTAGGCACCACAACTTGAGT-TGGAAATTTTGCTGCTTGAAGCTTCAGCCCTGACC 1798
 Qy 1799 CTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAG 1858
 || || ||| || ||||| | ||||| ||||| ||||| || || |||
 Db 1799 CTCTGCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTC---CTTCCAG 1854
 Qy 1859 AAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGA 1918
 ||||| ||| || ||| ||| ||| ||||| ||||| ||||| |||||
 Db 1855 AAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTGTGGTACCCTGGCAGAGA 1913
 Qy 1919 AGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTA 1978
 | | ||| | | ||||| ||||| ||||| || ||| | || ||||| |
 Db 1914 AAGGGCCAATC-TCATTCCTGCTGGCCAAAGTCAGCAGAAGAAGGTG--AAGTTTGCCA 1970
 Qy 1979 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2038
 ||||| || ||||| | | ||||| ||| ||| ||||| ||| |||
 Db 1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAAGACTGCGTCTT 2029
 Qy 2039 GAATTAATAAAAAAAAA 2052
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 Db 2030 GAGATAAACAAGAA 2043

RESULT 13

US-09-548-372D-29

; Sequence 29, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 29

; LENGTH: 1362

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 65.7%; Score 1359; DB 4; Length 1362;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Db	1	ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC	60
Qy	61	GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Db	61	GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780

Qy 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
 |||
 Db 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
 |||
 Db 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
 |||
 Db 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy 961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT 1020
 |||
 Db 961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT 1020

Qy 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
 |||
 Db 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
 |||
 Db 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
 |||
 Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
 |||
 Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320
 |||
 Db 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG 1320

Qy 1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359
 |||
 Db 1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA 1359

RESULT 14

US-09-548-367D-29

; Sequence 29, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-29

Query Match 65.7%; Score 1359; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
        |||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
        |||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
        |||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        |||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359

RESULT 15

US-09-551-853D-29

; Sequence 29, Application US/09551853D

; Patent No. 6500667

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; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-29

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Query Match          65.7%; Score 1359; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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Gapop 10.0 , Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2070	100.0	2070	9	US-09-794-748-3	Sequence 3, Appli
5	2070	100.0	2070	9	US-09-794-925-3	Sequence 3, Appli
6	2070	100.0	2070	9	US-09-681-442-3	Sequence 3, Appli
7	2070	100.0	2070	11	US-09-869-414-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1

US-09-794-927-3

; Sequence 3, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

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; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-927-3

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
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US-09-795-847-3

; Sequence 3, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 2070

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-795-847-3

Query Match 100.0%; Score 2070; DB 9; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080

Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAAACCTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAAACCTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTAAGTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980

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Db      1921 AGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
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Qy      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
          |||
Db      1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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Qy      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
          |||
Db      2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

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RESULT 3

US-09-794-743-3

; Sequence 3, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 2070

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-794-743-3

Query Match 100.0%; Score 2070; DB 9; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60
          |||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCCAC 60
          |||
Qy      61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db	61	GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG	120
Qy	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Db	121	CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT	180
Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGAT	960

Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800

Qy 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
 |||
 Db 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
 Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 |||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 |||
 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 4

US-09-794-748-3

; Sequence 3, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280JL

; CURRENT APPLICATION NUMBER: US/09/794,748

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 2070

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-794-748-3

Query Match

100.0%; Score 2070; DB 9; Length 2070;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
      |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
      |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
      |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300
      |||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
      |||
Db    301 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
      |||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480
      |||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
      |||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
      |||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
      |||
Db    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
      |||
Db    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720

Qy    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
      |||
Db    721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy    781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
 Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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 Db 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
 Qy 961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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 Db 961 GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
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 Db 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
 Qy 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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 Db 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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 Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
 Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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 Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
 Qy 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG 1320
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 Db 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG 1320
 Qy 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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 Db 1321 GAAGACTGTGGCTACAACATTCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
 Qy 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG 1440
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG 1440
 Qy 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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 Db 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
 Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
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 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
 Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
 |||||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
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 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
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 Db 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
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 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
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 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 5

US-09-794-925-3

; Sequence 3, Application US/09794925

; Patent No. US20020064819A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280HI

; CURRENT APPLICATION NUMBER: US/09/794,925

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-925-3

Query Match 100.0%; Score 2070; DB 9; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

Qy    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT 480

Qy    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540

Qy    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy    661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGGTATC 720
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Db	661	CCCCCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560

Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
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 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1801 TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1921 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
 ||||||||||||||||||||||||||||
 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 6

US-09-681-442-3

; Sequence 3, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

```
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2070
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-681-442-3
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Db 541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600

Qy 601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db 601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660

Qy 661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC 720
 |||

Db 661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGGAGCATGATCATTGGAGGTATC 720

Qy 721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
 |||

Db 721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780

Qy 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
 |||

Db 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840

Qy 841 TACAACATATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
 |||

Db 841 TACAACATATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900

Qy 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Db 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960

Qy 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020
 |||

Db 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT 1020

Qy 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
 |||

Db 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080

Qy 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140

Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
 |||

Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200

Qy 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260
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Db 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260

Qy 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG 1320
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Db 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATG 1320

Qy 1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380
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Db 1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380

Qy 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG 1440
 |||

Db 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGAGTGG 1440

Qy 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
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 Db 1441 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500

Qy 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
 |||
 Db 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560

Qy 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620
 |||
 Db 1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620

Qy 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680
 |||
 Db 1621 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG 1680

Qy 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740
 |||
 Db 1681 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT 1740

Qy 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT 1800
 |||
 Db 1741 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT 1800

Qy 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860
 |||
 Db 1801 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA 1860

Qy 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
 |||
 Db 1861 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920

Qy 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
 |||
 Db 1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980

Qy 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
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 Db 1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040

Qy 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070
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 Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2070

RESULT 7

US-09-869-414-3

; Sequence 3, Application US/09869414

; Publication No. US20030077226A1

; GENERAL INFORMATION:

; APPLICANT: Beinkowski et al.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280M

; CURRENT APPLICATION NUMBER: US/09/869,414

Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380

Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Db	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Db	1801	TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA	1860
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

RESULT 8

US-09-548-366-3

; Sequence 3, Application US/09548366

; Publication No. US20030104365A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

```

; APPLICANT:  Heinrikson, Robert L.
; APPLICANT:  Parodi, Luis A.
; APPLICANT:  Yan, Riqiang
; TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION:  USES THEREFOR
; FILE REFERENCE:  28341/6280A
; CURRENT APPLICATION NUMBER:  US/09/548,366
; CURRENT FILING DATE:  2000-04-12
; PRIOR APPLICATION NUMBER:  60/155,493
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  09/404,133
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  PCT/US99/20881
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  60/101,594
; PRIOR FILING DATE:  1998-09-24
; NUMBER OF SEQ ID NOS:  65
; SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-366-3

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Query Match          100.0%; Score 2070; DB 11; Length 2070;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db      1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
        |||
Db     61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
        |||
Db    121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
        |||
Db    181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300
        |||
Db    241 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA 300

Qy    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360
        |||
Db    301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
        |||
Db    361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420

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Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTCTTTGACTCT	600
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320

Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1501	 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1561	 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1621	 CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1681	 GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Db	1741	 CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT	1800
Qy	1801	TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1801	 TTGTCCACCATTCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Qy	1861	GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Db	1861	 GTA CTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920
Qy	1921	AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Db	1921	 AGACCAAGCTTGTTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT	1980
Qy	1981	TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Db	1981	 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA	2040
Qy	2041	ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070
Db	2041	 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2070

Db 301 GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360

Qy 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Db 361 TACCGGGACCTCCGGAAGGGTGTGTATGAGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 420
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Qy 421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT 480
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Db 421 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT 480
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Qy 481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
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Db 481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG 540
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Qy 541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Db 541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT 600
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Qy 601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 660
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Db 601 CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC 660
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Qy 661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
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Db 661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC 720
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Qy 721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Db 721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780
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Qy 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Db 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840
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Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
 |||

Db 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA 900
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Qy 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
 |||

Db 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 960
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Qy 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT 1020
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Db 961 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATT 1020
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Qy 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Db 1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080
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Qy 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Db 1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140
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Qy 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Db 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200
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Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1261	CATGTGCACGATGAGTTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Db	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGTCAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTTC	1559
Db	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTTC	1560
Qy	1560	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1619
Db	1561	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTC	1620
Qy	1620	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1679
Db	1621	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1680
Qy	1680	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1739
Db	1681	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC	1740
Qy	1740	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACC	1799
Db	1741	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACC	1800
Qy	1800	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1859
Db	1801	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGA	1860
Qy	1860	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA	1919
Db	1861	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCGGGCAGAGAA	1920
Qy	1920	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1979
Db	1921	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1980
Qy	1980	TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG	2039
Db	1981	TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG	2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059
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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 10

US-10-308-365-1

; Sequence 1, Application US/10308365
; Publication No. US20030109022A1
; GENERAL INFORMATION:
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: MURPHY, KAY
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SMITH, TRUDI S.
; TITLE OF INVENTION: ASP 2
; FILE REFERENCE: GH-70368-2
; CURRENT APPLICATION NUMBER: US/10/308,365
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/694,200
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: UK 9701684.4
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 09/009,191
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE: FEATURE: MISCELLANEOUS FEATURE
; NAME/KEY: UNSURE
; LOCATION: (2455) (2456) (2463) (2478) (2480) (2497) (2507) (2509) (2512) (2516) (2520)
; LOCATION: (2522) (2525) (2529) (2539) (2540)
; OTHER INFORMATION: OTHER INFORMATION: n= a, g, c or t
US-10-308-365-1

Query Match 98.2%; Score 2032; DB 15; Length 2541;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120
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Db 61 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG 120

Qy 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180
| | | | | | | | | | | | | | | | | |
Db 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGAGGGGCAGCTTT 180

Qy 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240
| | | | | | | | | | | | | | | | | |
Db 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 240

Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACCTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Qy	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	601	CTGGTAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Qy	781	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	781	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140

Db	1081	 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1141	 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1201	 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Db	1261	 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACACCTTGGACATG	1320
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1321	 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1381	 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1441	 CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT-GGACCACACCTCCGTGGTTTC	1559
Db	1501	 AAGTGAGGAGGCCCATGGGAGAAAAGATAGAGATTCCCCTGGGACCACACCTCCGTGGTTTC	1560
Qy	1560	ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTC	1619
Db	1561	 ACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCCTC	1620
Qy	1620	CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1679
Db	1621	 CCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCA	1680
Qy	1680	GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATAC	1739
Db	1681	 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATAC	1740
Qy	1740	TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC	1799
Db	1741	 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC	1800
Qy	1800	TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA	1859
Db	1801	 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGA	1860
Qy	1860	AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA	1919
Db	1861	 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAA	1920
Qy	1920	GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT	1979

Db 1921 GAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTGCTAT 1980

Qy 1980 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2039
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Db 1981 TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 2040

Qy 2040 AATTAAAAAAAAAAAAAAAAA 2059
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Db 2041 AATTAAAAAAAAAACTAGA 2060

RESULT 11

US-09-796-264-1

; Sequence 1, Application US/09796264
 ; Patent No. US20020049303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Jordan J.N.
 ; APPLICANT: Lin, Xinli
 ; APPLICANT: Koelsch, Gerald
 ; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
 ; TITLE OF INVENTION: of Use Thereof
 ; FILE REFERENCE: OMRF 179
 ; CURRENT APPLICATION NUMBER: US/09/796,264
 ; CURRENT FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 09/604,608
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/168,060
 ; PRIOR FILING DATE: 1999-11-30
 ; PRIOR APPLICATION NUMBER: 60/177,836
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 60/178,368
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: 60/210,292
 ; PRIOR FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-796-264-1

Query Match 97.1%; Score 2010; DB 9; Length 3252;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
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Db 1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy 100 CTGGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 159
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Db 61 CTGGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 120

Qy 160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
 |||

Db 121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATAACGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	420
Qy	460	GTCACCTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCACCTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAACCTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCCTGACGACTCC	579
Db	481	TCCAACCTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCCGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020

Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA	1959

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Db      1861  |||||TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTCCTGCTGGCCAAAGTCAGTAGGA 1920
Qy      1960  GAGGATGCACAGTTTGTCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
Db      1921  |||||GAGGATGCACAGTTTGTCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980
Qy      2020  GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
Db      1981  |||||GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 12

US-09-845-226-1

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; Sequence 1, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-845-226-1

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Query Match          97.1%; Score 2010; DB 10; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      40  GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
Db      1   GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy     100  CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 159
Db      61  CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 120

Qy     160  CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
Db     121  CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

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Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAAC	420
Qy	460	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACAGTCTGAAGTGTGGCCTCTGTGCGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACAGTCTGAAGTGTGGCCTCTGTGCGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020

Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
Db	1081	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1959

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Db      1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920
Qy      1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019
Db      1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980
Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAACAAAAAAAAAAAAA 2057
Db      1981 GGTGCAAAGATTGCCTCTTGAATTAACAAAAAACTAGA 2018

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RESULT 13

US-09-795-903A-1

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; Sequence 1, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-903A-1

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Query Match          97.1%; Score 2010; DB 10; Length 3252;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
Db      1  GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60
Qy     100 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 159
Db      61 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAG 120
Qy     160 CCCGGCCGGAGGGGCGAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGGCGAG 219

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Db	121	CCCGGCCGGAGGGGAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG	180
Qy	220	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	279
Db	181	GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT	240
Qy	280	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACCTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	420
Qy	460	GTCCTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCCTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACCTATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020

Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179
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Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	GGCTTTGCTGTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	CAGAGCACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1899
Db	1801	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTACCTTGGCGTGTGTCCC	1860

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Qy      1900 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959
          |||
Db      1861 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1920

Qy      1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAAACAAGCCTAACATT 2019
          |||
Db      1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAAACAAGCCTAACATT 1980

Qy      2020 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAAAAAAAAA 2057
          |||
Db      1981 GGTGCAAAGATTGCCTCTTGAATTAATAAAAAAACTAGA 2018

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RESULT 14

US-10-032-818-1

; Sequence 1, Application US/10032818

; Publication No. US20030092629A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Jordan J.N.

; APPLICANT: Koelsch, Gerald

; APPLICANT: Ghosh, Arun K.

; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof

; FILE REFERENCE: 2932.1006-007

; CURRENT APPLICATION NUMBER: US/10/032,818

; CURRENT FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: US 60/275,756

; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: US 60/258,705

; PRIOR FILING DATE: 2000-12-28

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 3252

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-032-818-1

Query Match 97.1%; Score 2010; DB 15; Length 3252;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
          |||
Db      1 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 60

Qy      100 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 159
          |||
Db      61 CTGGGGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAG 120

Qy      160 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219
          |||
Db      121 CCCGGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 180

Qy      220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
          |||
Db      181 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 240

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Qy	280	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	339
Db	241	ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTAC	300
Qy	340	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	399
Db	301	CAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC	360
Qy	400	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	459
Db	361	CAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAAC	420
Qy	460	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	519
Db	421	GTCAGTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGC	480
Qy	520	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	579
Db	481	TCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC	540
Qy	580	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	639
Db	541	CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG	600
Qy	640	CACCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	699
Db	601	CAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGGAGGG	660
Qy	700	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	759
Db	661	AGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCC	720
Qy	760	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	819
Db	721	ATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGAT	780
Qy	820	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	879
Db	781	CTGAAAATGGACTGCAAGGAGTACAACATATGACAAGAGCATTGTGGACAGTGGCACCACC	840
Qy	880	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	939
Db	841	AACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCC	900
Qy	940	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	999
Db	901	TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCA	960
Qy	1000	GGCACCACCCCTTGGAACATTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1059
Db	961	GGCACCACCCCTTGGAACATTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC	1020
Qy	1060	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1119
Db	1021	AACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG	1080
Qy	1120	GCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTT	1179

Db	1081	 GCCACGTCCCAAGACGACTGTTACAAGTTTGGCATCTCACAGTCATCCACGGGCACTGTT	1140
Qy	1180	ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1239
Db	1141	 ATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATT	1200
Qy	1240	GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1299
Db	1201	 GGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGC	1260
Qy	1300	CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1359
Db	1261	 CCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCA	1320
Qy	1360	ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1419
Db	1321	 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTC	1380
Qy	1420	TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1479
Db	1381	 TGCCTCATGGTGTGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTT	1440
Qy	1480	GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1539
Db	1441	 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT	1500
Qy	1540	GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1599
Db	1501	 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGC	1560
Qy	1600	CAGAGCACCTCAGGACCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1659
Db	1561	 CAGAGCACCTCAGGACCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAA	1620
Qy	1660	GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1719
Db	1621	 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAG	1680
Qy	1720	CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1779
Db	1681	 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT	1740
Qy	1780	TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1839
Db	1741	 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT	1800
Qy	1840	CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGCGGTGTGTCCC	1899
Db	1801	 CTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGCGGTGTGTCCC	1860
Qy	1900	TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1959
Db	1861	 TGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA	1920
Qy	1960	GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATT	2019

Db 1921 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 1980

Qy 2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAAAAAAAAAAAA 2057
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Db 1981 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAACTAGA 2018

RESULT 15

US-09-794-927-5

; Sequence 5, Application US/09794927
 ; Patent No. US20010016324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Bienkowski, Michael J.
 ; APPLICANT: Heinrikson, Robert L.
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Yan, Riqiang
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND
 ; TITLE OF INVENTION: USES
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 28341/6280FG
 ; CURRENT APPLICATION NUMBER: US/09/794,927
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 09/416,901
 ; PRIOR FILING DATE: 1999-10-13
 ; PRIOR APPLICATION NUMBER: 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1977
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-794-927-5

Query Match 91.2%; Score 1887.2; DB 9; Length 1977;
 Best Local Similarity 96.2%; Pred. No. 0;
 Matches 1974; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

Qy 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60
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Db 1 ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC 60

Qy 61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120
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Db 61 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGG 120

Qy 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180
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Db 121 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT 180

Qy	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Db	181	GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC	240
Qy	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Db	241	GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA	300
Qy	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Db	301	GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA	360
Qy	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Db	361	TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG	420
Qy	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAAACATT	480
Db	421	CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCCTGTGCGTGCCAAACATT	480
Qy	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Db	481	GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG	540
Qy	541	GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT	600
Db	541	GGGCTGGCCTATGCTGAGATTGCCAGG-----	567
Qy	601	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC	660
Db	568	-----CTTTGTGGTGCTGGCTTC	585
Qy	661	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	720
Db	586	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCTGGAGGGAGCATGATCATTGGAGGTATC	645
Qy	721	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	780
Db	646	GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT	705
Qy	781	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	840
Db	706	GAGGTGATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	765
Qy	841	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	900
Db	766	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	825
Qy	901	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	960
Db	826	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	885
Qy	961	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	1020
Db	886	GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT	945

Qy	1021	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1080
Db	946	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC	1005
Qy	1081	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1140
Db	1006	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	1065
Qy	1141	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1200
Db	1066	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	1125
Qy	1201	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1260
Db	1126	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	1185
Qy	1261	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1320
Db	1186	CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG	1245
Qy	1321	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1380
Db	1246	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	1305
Qy	1381	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1440
Db	1306	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAAGTGG	1365
Qy	1441	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1500
Db	1366	CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG	1425
Qy	1501	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1560
Db	1426	AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA	1485
Qy	1561	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1620
Db	1486	CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC	1545
Qy	1621	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1680
Db	1546	CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG	1605
Qy	1681	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1740
Db	1606	GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACT	1665
Qy	1741	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1800
Db	1666	CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCT	1725
Qy	1801	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1860
Db	1726	TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA	1785
Qy	1861	GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG	1920

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Db    1786 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1845

Qy    1921 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1980
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1846 AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT 1905

Qy    1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1906 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 1965

Qy    2041 ATTAAAAAAAAA 2052
      | |||||||||
Db    1966 AAAAAAAAAA 1977

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Search completed: January 21, 2004, 20:26:49
Job time : 707 secs